



Sequence	1638 AA;	XX	XX	Sequence	758 AA;	XX	XX	Sequence	758 AA;	XX	XX
Query Match	10.2%; Score 138; DB 4; Length 1638;			Query Match	9.2%; Score 125; DB 4; Length 758;			Query Match	9.2%; Score 125; DB 4; Length 758;		
Best Local Similarity	21.2%; Pred. No. 0.00033; Mismatches 100; Indels 72; Gaps 13;			Best Local Similarity	25.6%; Pred. No. 0.0025; Mismatches 93; Indels 62; Gaps 13;			Best Local Similarity	25.6%; Pred. No. 0.0025; Mismatches 93; Indels 62; Gaps 13;		
Matches	58; Conservative 43; Mismatches 100; Indels 72; Gaps 13;			Matches	62; Conservative 25; Mismatches 93; Indels 62; Gaps 13;			Matches	62; Conservative 25; Mismatches 93; Indels 62; Gaps 13;		
QY	3 KILVGFAAREVVAISADSVHRCILSACILNAAFDTFGFECESVWVYDPAECINTEDRDRPDLF 62			QY	21 CLSACINAADFDTGFBCESVWVYDPAECIL-NTEDRDRPDLFVDEDEHDTVTYLDNNCA 78			QY	21 CLSACINAADFDTGFBCESVWVYDPAECIL-NTEDRDRPDLFVDEDEHDTVTYLDNNCA 78		
Db	211 KLPISDIKEITAANR-SDCEKCLN--EFSFVCRSANFDSTMRSCTLSRTRTHPELM 266			Db	160 CLEAC----QANESCSAVNY--ETGLCVMFRSTADOLP-GSLSRSQIYVFTVIAQKSCF 211			Db	160 CLEAC----QANESCSAVNY--ETGLCVMFRSTADOLP-GSLSRSQIYVFTVIAQKSCF 211		
QY	63 VDHEPDIVYLDNNAGCCCHWHDNPKTSIGLNDQQFIAQCYAQCYVQYAVEGROL 122			QY	267 EDDPNSD-YYLENTCLNAE-----RRCG-----LAVFVKEENKL 300			QY	267 EDDPNSD-YYLENTCLNAE-----RRCG-----LAVFVKEENKL 300		
Db	267 EDDPNSD-YYLENTCLNAE-----RRCG-----LAVFVKEENKL 300			QY	123 SD--BLDHSPEGELSEFELCTORLSVTANDFNCKSFMSNLTRSCVLSRS-RLPLGR 179			QY	123 SD--BLDHSPEGELSEFELCTORLSVTANDFNCKSFMSNLTRSCVLSRS-RLPLGR 179		
QY	301 GGPFEVD-1FNNTMELECOTMC---LRAEKVFCRSVERDDQSKQCLISEEDSISQKD 354			Db	355 ISISSSPTHFYDVLVCLDNQRANDYPDNSVTSILHFLSSGRRPDTAQQVYRNSRLGGEFHSE 414			Db	355 ISISSSPTHFYDVLVCLDNQRANDYPDNSVTSILHFLSSGRRPDTAQQVYRNSRLGGEFHSE 414		
QY	180 ANLAEVPGTYFE-----SRGVSPFTRVQMLVNG-RASP 213			QY	214 VMENVPSTVIMCLQOCTSPPTGONFVCKSVMY 246			Db	195 GV-PS---FTRVQMLVNGFASFVMENVPSTMCLQOCTSPPTGONFVCKSVMY 248		
QY	415 ITGR--SUSECLUBCLRQ----TSFQCRSAVY 440			QY	299 CAERPSKLCEFPKRVAGRLKTVDS-VHQNQVQIDECDRLCLTAP-----FRCHS-YD 349			Db	299 CAERPSKLCEFPKRVAGRLKTVDS-VHQNQVQIDECDRLCLTAP-----FRCHS-YD 349		
Db	415 ITGR--SUSECLUBCLRQ----TSFQCRSAVY 440			QY	249 NE 250			Db	249 NE 250		
RESULT 2				Db	350 NE 351			Db	350 NE 351		
ID	ABB58337 standard; protein; 758 AA..			RESULT 3				Db	350 NE 351		
XX	ABB58337;			ID	ABB58425			Db	350 NE 351		
AC	ABB58337;			ID	ABB58426			Db	350 NE 351		
XX	26-MAR-2002 (first entry)			AC	ABB58426;			Db	350 NE 351		
DE	Drosophila melanogaster polypeptide SEQ ID NO 1803.			XX	26-MAR-2002 (first entry)			Db	350 NE 351		
XX	Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.			XX	Drosophila melanogaster polypeptide SEQ ID NO 2070.			Db	350 NE 351		
KW	Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.			XX	Drosophila melanogaster polypeptide SEQ ID NO 2070.			Db	350 NE 351		
OS	Drosophila melanogaster.			XX	Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.			Db	350 NE 351		
XX	WO200171042-A2.			XX	Drosophila melanogaster.			Db	350 NE 351		
PD	27-SEP-2001.			XX	WO200171042-A2.			Db	350 NE 351		
XX	23-MAR-2001; 2001WO-US009231.			XX	PD	27-SEP-2001.		Db	350 NE 351		
PR	23-MAR-2000; 2000US-0191637P.			XX	PD	27-SEP-2001.		Db	350 NE 351		
PR	11-JUL-2000; 2000US-00614150.			XX	PR	23-MAR-2001; 2001WO-US009231.		Db	350 NE 351		
XX	(PEKE ) PE CORP NY.			XX	PR	23-MAR-2000; 2000US-0191637P.		Db	350 NE 351		
PA	WO200171042-A2.			XX	PR	11-JUL-2000; 2000US-00614150.		Db	350 NE 351		
XX	PT			XX	PA	(PEKE ) PE CORP NY.		Db	350 NE 351		
PT	Venter JC, Adams M, Li PWD, Myers EW;			XX	PA	(PEKE ) PE CORP NY.		Db	350 NE 351		
XX	WPI; 2001-556860/75.			XX	PT	Venter JC, Adams M, Li PWD, Myers EW;		Db	350 NE 351		
DR	N-PSDB; ABL02440.			XX	PT	Venter JC, Adams M, Li PWD, Myers EW;		Db	350 NE 351		
PS	Disclosure; SEQ ID NO 1803; 21pp + sequence Listing; English.			XX	DR	WPI; 2001-556860/75.		Db	350 NE 351		
XX	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.			XX	DR	N-PSDB; ABL02529.		Db	350 NE 351		
PT	PT			XX	PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.		Db	350 NE 351		
XX	PT			XX	PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.		Db	350 NE 351		
PS	Disclosure; SEQ ID NO 2070; 21pp + sequence Listing; English.			XX	PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.		Db	350 NE 351		
XX	PT			XX	PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.		Db	350 NE 351		
CC	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL0501), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL57737-ABL7072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly			CC	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL0501), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL57737-ABL7072).			CC	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL0501), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL57737-ABL7072).		

CC ABB72072]. The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)  
 XX SQ Sequence 744 AA;

Query Match 8.9%; Score 121; DB 4; Length 744;  
 Best Local Similarity 23.4%; Pred. No. 0.0061; Mismatches 102; Indels 78; Gaps 14;  
 Matches 64; Conservative 29; Mismatches 102; Indels 78; Gaps 14;  
 Qy 5 LVGFVAREVVA-----DS-----VHRCISACLNADFTRGPFECBSVMMYPVDAEC 43  
 Db 117 LVGF-----EIVGIVFSAPEKLMDSQPGTLMIDCLDTCRK-----NKTQSVNY-----ETGLC 167  
 Qy 49 ILVNTEDRLRPP-----LVDNERHDTVIYLDDNNGAG-----CECHWHFDKFTSGILNDQFATAA 104  
 Db 168 VLFSAHADOLPGLALKSQQFVFTIQAQKSLAVKPCRSRAWYDR----- 211  
 Qy\* 105 QCAYAPVTVQVAVEGRQLSDELDHISFEGEGLSCEELCTORLSVTANDNCNSKMSNLT 164  
 212 -----VQVYKLTKEVKRVSVASRRECELC-----LGENDFTCRSANYDRS 254  
 Qy 165 RSCVLSDERSRPLGRNLAEV-----PSGTYFESRGVP-----SFRVQPMQMLVGFASPMEN 217  
 Db 255 GACELSELDRLLTAGSQAFQVNDGSDYLENHCVDENPKLCEFKRLUPGRILKTVDS-VYOE 313  
 Qy 218 VPSVVMCLQDCTSPPETGONFVCKSVMYNE 250  
 Db 314 VSIDECRELCLNSP-----YRCHS-----YDYN 338

CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL0180-ABL16175) and the encoded proteins (ABR57737-  
 CC ABB72072]. The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

SQ Sequence 692 AA;

Query Match 8.9%; Score 120.5; DB 4; Length 692;  
 Best Local Similarity 19.9%; Pred. No. 0.0062; Mismatches 92; Indels 87; Gaps 9;  
 Matches 53; Conservative 35; Mismatches 92; Indels 87; Gaps 9;  
 Qy 3 KILVGFVAREVVSADSVHRCISACLNADFTRGPFECBSVMMYPVDAECILNTEDRLRDPDLP 62  
 Db 118 KVIRGLDNALIYVSTKELACLSACIN-----ERRFVCRSVEFVSDYNNKCVLSDSRSSGQEV 174  
 Qy 63 VDEHEBDTVYLDNNGC-----AGCECHWHFDKFTSGILNDQFATAAQCYAPYTVQVAVAE 118  
 Db 175 OLIVDQGTDIFENCLKPKAQACKNSRFSNSQNGMVSEK-----VAQIVGL- 221  
 Qy 119 GRQLSDELDHISFEGEGLSCEELCTORLSVTANDNCNSKMSNLTR----- 165  
 Db 222 -----HYVTDKELQVTSSEACRLACIESEBLFLCRSFLYQGQPSQNCYRCLYHLDH 272  
 Qy 166 -----SCVLSDERSRPLGRNLAEV-----PSGTYFESRGVP-----GVSFTRVHQ 204  
 Db 273 KTLPGPSVSYLNHERRPLDNGEPIGQ-----YFENQCKAAGLGLAGSPPGT--- 318  
 Qy 205 MLVGFASFTMENYPSVTCMLQDCTSP 231  
 Db 319 -----LDKIDTLPSLDTEDP 335

SQ Sequence 692 AA;

RESULT 4  
 ABB70535 standard; protein; 692 AA.

XX AC ABB70535;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 38397.

XX KW Drosophila; developmental biology; cell signalling; insecticide;

XX KW pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO20171042-A2.

XX PD 27-SEP-2001.

XX XW 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE ) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-65660/75.

XX DR N-PSDB; ABL14638.

XX PS Disclosure; SEQ ID NO 38397; 21pp + Sequence Listing; English.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 CC genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions.

XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 useful in developmental biology and in elucidating cell signalling and  
 cell-cell interactions in higher eukaryotes for the development of  
 insecticides, therapeutics and pharmaceutical drugs. The invention

SQ Sequence 692 AA;

SQ Sequence 692 AA;

RESULT 5  
 AAG67230 standard; protein; 790 AA.

XX AC AAG67230;

XX DT 13-NOV-2001 (first entry)

XX DE Amino acid sequence of pig plasminogen.

XX KW Angiostatin; plasminogen; sulphydryl donor; angiogenesis; tumour;

XX KW angiogenic disease; neoplastic disease; connective tissue disorder;

XX KW rheumatoid arthritis; atherosclerosis; ocular angiogenic disease;

XX KW diabetic retinopathy; corneal graft rejection; cardiovascular disease;

XX KW cerebral vascular disease; diabetes; immune disorder;

XX KW chronic inflammation; autoimmunity.

XX OS Sus scrofa.

XX PN WO20158921-A2.

XX PR 16-AUG-2001.

XX PR 08-FEB-2001; 2001WO-US004021.

XX PR 08-FEB-2000; 2000US-00500397.

XX PA (NOUN ) UNIV NORTHWESTERN.

XX PI Sofe G, Gately ST, Twardowski P;

XX DR WPI; 2001-550019/51.

XX PS Disclosure; Page 77-80; 101pp; English.

PT Producing angiostatin for treating angiogenic disease involves  
 PT contracting plasminogen with plasminogen activator and sulphydryl donor  
 PT simultaneously, or producing plasmin which is contacted with sulphydryl  
 XX donor.

XX Disclosure; Page 77-80; 101pp; English.

CC The specification describes a method for generating angiostatin in vitro.  
 CC The method comprises contacting plasminogen with a sulfonyl donor, or  
 CC culturing cells capable of producing plasminogen activator in conditioned  
 CC culture medium (CM) and contacting the CM with plasminogen. Angiostatin  
 CC produced by method of the invention is useful for treating animals with  
 CC angiogenesis diseases. It is useful for treating an angiogenic disease  
 CC such as neoplastic diseases (e.g. tumours and tumour metastasis), benign  
 CC tumours (e.g. hemangiomas, acoustic neuromas, etc), connective tissue  
 CC disorders (e.g. rheumatoid arthritis and atherosclerosis), ocular  
 CC angiogenic diseases (e.g. diabetic retinopathy, corneal graft rejection,  
 CC etc), cardiovascular diseases, cerebral vascular diseases, diabetes-  
 CC associated diseases and immune disorders (e.g. chronic inflammation and  
 CC autoimmunity). The present sequence represents a plasminogen  
 XX sequence 790 AA;  
 SQ

Query Match 8.6%; Score 116; DB 4; Length 790;  
 Best Local Similarity 19.5%; Pred. No. 0.021; Mismatches 100; Indels 84; Gaps 12;

Matches 55; Conservative 43; Mismatches 100; Indels 84; Gaps 12;

QY 5 LVGFAREVNSADSVHRCLSACLNNAFDITFGFECESVMYYPVDAECLNTEDRDLRDPFLVD 64  
 Db 14 LFSLSRKQVAAKSVEECAAKC-EAET-NFICRFAQYHSKQDQCVVMAENSKTSP--IA 67  
 QY 65 EHEDTV----IYLDNNCAGCBECHWHFDNFKTSQGILNDQFQIAQCYAPYVQYAVEG 119  
 Db 68 RMRDVVLFEKRIYILSECKTNGKMYRGTTSKTSKGVCIQKNSVSPHPIKYSPEKPLAG 127  
 QY 120 RQ-----LSDELDHSTEGLESECECLCTQ-----RIVSTANDFNC 155  
 Db 128 LSENYCRNPNDBKGPWCYTDBTRFDYCDIPCEDECIMHICSGEHYEGKISKTMGIEC 187  
 QY 156 Ks-----PMYSNTRS-CVLSRSRSLGRANLAEVPGWTFYFESRGVPSF 199  
 Db 188 QWGSQSPHAGYGLPSKRPNKKMVKYCRNPQGPEPRP-----W-----CF 227  
 QY 200 TRVQMLLVGFASFVMEVPSVYMCUDQCTSPPPTCQNFYC 241  
 Db 228 TTDPN-----KRMFCDIP-----RCTIPPTSGPTYQC 256

RESULT 6

ABB58185  
 ID ABB58185 standard; protein; 833 AA.

AC ABB58185;  
 XX  
 DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 1347.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical.

OS Drosophila melanogaster.

XX  
 PN WO200171042-A2.

PD 27-SEP-2001.

XX  
 PF 23-MAR-2001; 2001WO-US0009231.

PR 23-MAR-2000; 2000US-0191337P.  
 11-JUL-2000; 2000US-00614150.

PA (PEKE ) PE CORP NY.

XX  
 PT Venter JC, Adams M, Li PWD, Myers EW;

XX  
 DR WPI; 2001-656860/75.

XX  
 DR N-PSDB; ABD02288.

PT New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signaling and cell-cell  
 PT interactions.

CC Disclosure: SEQ ID NO 1347; 21PP + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL1676-ABL3031), expressed DNA  
 CC sequences (ABL1840-ABL6175) and the encoded proteins (ABL5777-  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed Specification, but was obtained in electronic format directly  
 CC from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)

SQ Sequence 833 AA;

Query Match 8.3%; Score 113; DB 4; Length 833;  
 Best Local Similarity 23.2%; Pred. No. 0.046; Mismatches 98; Indels 76; Gaps 15;

Matches 63; Conservative 34; Mismatches 98; Indels 76; Gaps 15;

QY 3 KILVGPAREVNSADS-----VHRCLASCLNAFDITFGFECESVMYYPVDAECL- 50  
 Db 122 EILITGY--VLSASPKSMPLTPGMLMLTCLEAQS----NESCSAVY--EYGLCVIF 171  
 QY 51 -NTEDBLRDPFLVDEHEDRIVYLDNNCAG--CCHWHFDNFKTSQGILNDQFQIAQAC 106  
 Db 172 KITADKLP-GSLRSQSPFVFTIYAKSCGVRPQSKAWKIDR----- 212  
 QY 107 YAPYVTOQYAVAGEGRQLSDUDHSTEGLESECECLCTQSLSVTANDFNCFSMYSNLTRS 166  
 Db 213 -----VQYRILPENKVSQSVTSLSRDCLIC----LGBTEFTCRSANYVRHSGL 257  
 QY 167 CVLSD-ERRPLGRNLGRANLAEVPGWTFYFESGV-PS----FTRVQMLLVGFASFVMEWP 219  
 Db 258 CELSDMDRFLISAGGSVPEPYDGBYLENNCAEPSKLCEFKRISGKILKTVDS-VYQDIN 316  
 QY 220 SVTMCLDQCMISPPPBETGQIVFVCKSVMYVYNE 250  
 Db 317 TIDECDLCLNSP-----YRCHS--YDYN 339

RESULT 7

AAY50872  
 ID AAY50872 standard; protein; 812 AA.

AC AAY50872;

DE 24-FEB-2000 (first entry)

XX Bovine plasminogen protein fragment.

XX Plasminogen; bovine; thrombolytic agent; streptokinase; antigenic;  
 XX blood clot; heart attack; treatment.

XX  
 OS Bos taurus.

XX  
 PN WO957251-A2.

XX  
 PD 11-NOV-1999.

XX  
 PR 06-MAY-1999; 99WO-US010086.

XX  
 PR 06-MAY-1998; 98US-0084392P.

XX  
 PA (OKLA-) OKLAHOMA MEDICAL REBS FOUND.

XX  
 PI Zhang XC, Lin X, Tang JUN;

XX  
 DR WPI; 2000-052966/04.

PT New thrombolytic agents derived from modified humanized streptokinase,





XX	DE	Plasminogen protein for production of recombinant plasminogen.
XX	KW	Plasminogen; alpha-1-antitrypsin; AAT; argsepins; recombinant; stabilising protein.
XX	OS	Homo sapiens.
XX	FT	Key Location/qualifier <sup>B</sup>
XX	FT	Misc-difference 60 /note= "encoded by ACC"
XX	FT	Misc-difference 191 /note= "encoded by GAA"
XX	FT	Misc-difference 223 /note= "encoded by AAA"
XX	FT	Misc-difference 280 /note= "encoded by GCT"
XX	FT	Misc-difference 291 /note= "encoded by CTG"
XX	FT	Misc-difference 395 /note= "encoded by GSA"
XX	FT	Misc-difference 503 /note= "encoded by CAG"
XX	FT	Misc-difference 607 /note= "encoded by TCT"
XX	FT	Misc-difference 615 /note= "encoded by CAG"
XX	FT	Misc-difference 658 /note= "encoded by TAC"
XX	FT	Misc-difference 709 /note= "encoded by GCT"
XX	FT	US5648254-A.
XX	FT	PR 15-JUL-1994; 94US-00275076.
XX	PR	15-JAN-1988; 88US-00144357.
XX	PR	04-DEC-1989; 89US-00445302.
XX	PR	28-OCT-1991; 91US-00785865.
XX	PA	(ZYMO ) ZYMOGENETICS INC.
XX	PR	Kumar AA, Mulvihill ER;
XX	PR	WPI; 1997-372063/34.
XX	DR	N-PSDB; AATB95686.
XX	PT	production of recombinant plasminogen - by co-expression with plasminogen -processing or -stabilising protein.
XX	PT	Example 2; Fig 6A-D; 32pp; English.
XX	CC	This is the protein plasminogen. The encoding cDNA is used in a new process for the production of plasminogen where a first DNA sequence encoding plasminogen and at least one additional DNA sequence encoding a protein that processes or stabilises the plasminogen is introduced into a eukaryotic host cell. The protein is selected from alpha-1-antitrypsin (AAT) and its variants and Argsepins. Both the DNA sequences are operably linked to transcriptional promoter and terminator sequences. The host cell is cultured under conditions that allow the DNA sequences to be expressed and the recombinant plasminogen is isolated from the host cell. Co-expression of plasminogen and the protein gives increased yields of undegraded plasminogen
XX	PS	Sequence 810 AA;
XX	FT	RESULT 12
XX	ID	AAR60519
XX	ID	AAR60519 standard; protein; 790 AA.
XX	AC	AAR60519;
XX	XX	25-MAR-2003 (revised)
XX	DT	22-MAR-1995 (first entry)
XX	DE	Human 'Glu' plasminogen.
XX	KW	Serine protease; Factor-Xa; recognition site; Plasminogen; kringle; fusion protein cleavage; protein folding; primer; Polymerase chain reaction; amplification.
XX	OS	Homo sapiens.
XX	PN	WO9418227-A2.
XX	XX	18-AUG-1994.
XX	PD	04-FEB-1994; 94WO-DK000054.
XX	PR	04-FEB-1993; 93DK-00000130.
XX	PR	05-FEB-1993; 93DK-00000139.
XX	PR	03-DEC-1993; 93WO-GB002492.
XX	PA	(DENZ-) DEnzyme APS.
XX	PT	Thøgersen HC, Holtet TL, Etzerodt M;
XX	DR	WPI; 1994-279681/34.
XX	PT	Refolding of polypeptide molecules - using a cyclic process involving denaturing and renaturating conditions to produce a correctly folded prod.
XX	PT	Disclosure; Page 148-50; 202pp; English.
XX	CC	cDNA encoding kringle domains 1 and 4 of human plasminogen (full sequence given in AAR60519) was PCR amplified using primers given in AAQ71268-1. Amplified cDNA was linked to a sequence encoding the Factor-Xa cleavage site (given in AAR60503), subcloned in vector pCMVICH6 so that it was linked to a hexahistidine-encoding sequence and expressed in E. coli QX13. The fusion protein was purified on an Ni2+-activated RNA-agarose column. A cyclic procedure was used to obtain correctly folded recombinant protein. (Updated on 25-MAR-2003 to correct PN field.)
XX	Db	33 IASVTKQQLGASSIEBAAKCBEDB--FVGRAFQHNSKQEQCIVMAENKSSIIIR 89
XX	Db	60 DIFVDBHEDTVYLDNNCAGGECHWMFDNFKSGILNDQQPAIAQCYAPVTVAVEG 119
XX	Db	90 DYLFLERK--VTLSCBKTGNKGNYTGSCKNGITCOKNST--SPH----- 133
XX	Oy	120 RQISDELDHSFEGLE-----LSCBCLTQ----- 144
XX	Db	134 RIRFSPATHPBBGLENVCRYDNDQGPWYTTDBKRYVCDIECEB3GMHCSCGNY 193
XX	Oy	145 -RLSVDANDRCKS-----FMSNLTRSCVLSLSDRSRPLGRANLARVPG 187
XX	Db	194 DCRISKIMSGEACQWDSOSPAHAGTIPSCPFNKLKJKNYCRNPER-----BLRP 243
XX	Oy	188 WTYFESRGVPSTTRVQMLVGFASVMENTPSVIMLDQTSPPETGQFRC 241
XX	Db	244 W-----CFTTDPN-----KANECLDIF-----RCTTPSSGPTVQ 275

Qy 5 LVGPREVVSADSHRCCLSACLNAAFFDTGFECESVMYVDAECLINTEDR-----LDRP 59  
 Query Match 7.5%; Score 102; DB 2; Length 810;  
 Best Local Similarity 17.7%; Pred. No. 0.57;  
 Matches 52; Conservative 45; Mismatches 89; Indels 108; Gaps 12;

QY 5 LVGFAREVVSADSVRHQLSACIATNAFDTGFBCESVMYVPIVDAECLNTEDR---LDRPD 60 Query Match 7.5%; Score 101; DB 7; Length 480;  
 14 LFSVTKKQLAGGSIECAKEEDEB--FTCRAFOYHSKEQQVIMAENRKSSITMRD 70  
 Db 61 LVFDEDEHDVITVLDNNCAGCCHWHDNFKQSSGILNDQFATAOCYAPYVYAVEGR 120  
 QY 71 VVLFERK---VYSECKITNGKNGYRGTMSKTRNGITCOKWST---SPH-----R 114  
 Db 121 QLSDELDHSFEGLE-----LSECELTQ----- 144  
 QY 115 PRFSRPATHPSGLEENYCRNPNDPQCPWCTTDPEKRYDYCCDILBCEEECHCSEGYND 174  
 QY 145 -RLSVTANDFNCKS-----FMISNLTRS-CVLSDESRPLGRNLAEVG 187  
 Db 175 GKSITKMSGLCQAWMSQSOPSHANGYIIPSKFPRKLNKQYCRNPDRDLP----- 223  
 QY 188 WTYFESRGVPSTTRVPOMLVGFASFVMEVNSVMTMCLDOCSTSPPETGONFVC 241  
 Db 224 W-----CFTDPN-----KRWELCDIP-----RCTTPPPSSGPTYQC 255  
 RESULT 13  
 ABU64288 ABU64288 standard; protein: 480 AA.  
 XX AC ABU64288;  
 XX DT 11-MAR-2004 (first entry)  
 XX DE Human angiostatin protein.  
 XX AC Vector; rAV; recombinant adeno-associated viral vector;  
 XX KW anti-angiogenesis; PNP; angiogenesis; eye disorder; blindness;  
 XX DE retinal degeneration; macular degeneration; neovascularisation;  
 XX KW ophthalmological.  
 OS Homo sapiens.  
 XX PN WO2003080648-A2.  
 XX PD 02-OCT-2003.  
 XX PF 20-MAR-2003; 2003WO-US008667.  
 XX PR 20-MAR-2002; 2002US-0366114P.  
 XX PA (UYFL ) UNIV FLORIDA RES FOUND INC.  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Hauswirth WW, Campochiaro PA, Berns KI;  
 XX DR WPI; 2003-779243/73.  
 XX PT Novel adeno-associated viral vector comprising polynucleotide encoding  
 PT pigment epithelium-derived factor, useful for treating choroidal  
 XX neovascularization, blindness, loss of vision.  
 PS Claim 14; Page 37; OPP; English.  
 CC The present invention relates to an adeno-associated viral (AAV) vector  
 CC comprising a polynucleotide that comprises a nucleic acid segment that  
 CC encodes a choroidal or ocular neovascularisation inhibitory polypeptide  
 CC operably linked to a promoter that expresses the segment to produce the  
 CC polypeptide in a selected mammalian host cell. Such a vector is useful  
 CC for providing a choroidal or ocular neovascularisation inhibitor  
 CC polypeptide to a mammal, for use in the therapy of ocular  
 CC neovascularisation, choroidal neovascularisation, retinal  
 CC dysfunction, loss of vision, retinopathy, or blindness in a human.  
 CC The present sequence is a protein shown in the exemplification of the  
 CC invention.  
 XX Sequence 480 AA;

RESULT 14  
 ABB75942 ABB75942 standard; protein: 563 AA.  
 XX AC ABB75942;  
 XX DT 01-JUL-2002 (first entry)  
 XX DE Endothelial cell growth inhibitor, angiogenesis.  
 XX AC Plasminogen; angiogenesis; angiogenesis; inhibitor; tumour; antitumour;  
 XX KW cytostatic; antipsoriatic; dermatological; ophthalmological;  
 XX KW antidiabetic; antiarthritic; vulnerary; antiluler; antiatherosclerotic;  
 XX KW contraceptive; gene therapy; human.  
 OS Homo sapiens.  
 OS Synthetic.  
 PH Key Location/Qualifiers  
 PT peptide 1..32  
 PT /label= Signal\_peptide  
 PT Peptide 33..96  
 PT /label= Pre-activation\_peptide  
 PT Domain 97..560  
 PT /label= Kringles\_1-6  
 XX WO200220813-A2.  
 XX PD 14-MAR-2002.  
 XX PR 31-AUG-2001; 2001WO-EP010090.  
 XX PR 05-SEP-2000; 2000US-0230893P.  
 XX PA (KARO-) KAROLINSKA INNOVATIONS AB.  
 XX PI Cao Y;  
 XX DR WPI; 2002-362251/39.  
 XX PT Novel recombinant protein termed angiogenesis useful for treating tumor,  
 PT ulcer, comprises amino acid sequence corresponding to Kringles 1-5,  
 PT secretory signal peptide and pre-activation peptide of mammalian  
 PT plasminogen.  
 XX PS Claim 6; Fig 6; 63pp; English.

CC The present sequence is the protein sequence of a novel recombinant  
 CC endothelial cell growth inhibitor, termed angiogenesis, which comprises  
 CC the signal peptide and pre-activation peptide of plaminogen (see  
 CC ABB75939) in association with Kringle 1-5. Angiogenesis may also  
 CC include a C-terminal tumour-targetting peptide (see ABB75943-44).  
 CC Angiogenesis is claimed. In claimed methods, the peripheral and tumour-  
 CC in the preparation of a medicament for treating a tumour by preventing  
 angiogenesis (claimed). In claimed methods, the peripheral and tumour-  
 CC infiltrating lymphocytes, hepatocytes, epidermal cells, myocytes or other  
 CC somatic cells of a patient in need of anti-angiogenic therapy are  
 CC transfected with a viral (especially retroviral) vector comprising an  
 CC angiogenesis nucleic acid, and the transfected cells are then expanded  
 CC and implanted into the patient. Angiogenesis is useful for inhibiting  
 CC cancer metastasis, and for treating angiogenesis associated conditions  
 CC such as tumour growth e.g., cancer, diabetes, etc. It is also useful for  
 CC treating haemangioma, solid tumours, leukaemia, psoriasis, sclerodema,  
 CC arteriovenous malformations, rubosis, neovascular glaucoma, diabetic  
 CC retinopathy, arthritis, diabetic neovascular macular degeneration, wound  
 CC healing, peptic ulcer, intestinal adhesions, atherosclerosis, fractures, keloids,  
 CC angiogenesis, or scratch fever. The protein can also be used as a birth control agent  
 CC by preventing the vascularisation required for embryo implantation. The  
 CC half maximal concentration (EC50) of angiogenesis for inhibiting  
 CC endothelial cell proliferation is about 50 pM, compared with 100 nM for  
 CC angiostatin  
 XX sequence 563 AA;

Query Match 7.5%; Score 101; DB 5; Length 563;  
 Best local Similarity 18.0%; Pred. No. 0.44; Mismatches 53; Conservative 42; Indels 110; Gaps 13;  
 Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

QY 5 LVGFAREVVSADSVRCLSLACLNADTFGEPECEVSVMYYPVDAECLNTEDR----LDRP 59  
 Db 33 LFSVTKKQLGAGSIECAKCEDEBEE--FTCRAFOYHSKEQCVIMAENRKSSIIIR 89  
 SQ  
 QY 60 DLFVDEHEDTVYIDNNCAGCCEHHWFDNFKTSGLNDQOFAIAQCYAPYVYAVEG 119  
 Db 90 DVLFEKK--VYLSCKTGNGKVRGTMSKTKNGTCKWST---SPH----- 133  
 QY 120 RQLSDELDISFEGLE-----LSECELCIQT----- 144  
 Db 134 RPRSPATHSEGLBENYCRNPNDPQGPWCYTDPKRYDYCILECBECHMCSEGVY 193  
 QY 145 --RLSVTANDPNC-----FMSNLTRS-CVLSDRSPPLGRANLAEPV 186  
 Db 194 DGKSKTMSGLEQAWDSOPSPAHGYIIPSKFPPKNNLKKNYCRNPDRRLRP----- 243  
 QY 187 GWTYFESRGVPSFTRVQPMILVGFFASFVMEVNPVSTMCIDQCTSPPPEQCNFVC 241  
 Db\* 244 -W-----CFTTDPN----KRWELCDIP-----RCTTPPSSGPTYOC 275  
 SQ

Query Match 7.5%; Score 101; DB 2; Length 566;  
 Best local Similarity 18.0%; Pred. No. 0.45; Mismatches 53; Conservative 42; Indels 110; Gaps 13;  
 Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

QY 5 LVGFAREVVSADSVRCLSLACLNADTFGEPECEVSVMYYPVDAECLNTEDR----LDRP 59  
 Db 33 LFSVTKKQLGAGSIECAKCEDEBEE--FTCRAFOYHSKEQCVIMAENRKSSIIIR 89  
 QY 60 DLFVDEHEDTVYIDNNCAGCCEHHWFDNFKTSGLNDQOFAIAQCYAPYVYAVEG 119  
 Db 90 DVLFEKK--VYLSCKTGNGKVRGTMSKTKNGTCKWST---SPH----- 133  
 QY 120 RQLSDELDISFEGLE-----LSECELCIQT----- 144  
 Db 134 RPRSPATHSEGLBENYCRNPNDPQGPWCYTDPKRYDYCILECBECHMCSEGVY 193  
 QY 145 --RLSVTANDPNC-----FMSNLTRS-CVLSDRSPPLGRANLAEPV 186  
 Db 194 DGKSKTMSGLEQAWDSOPSPAHGYIIPSKFPPKNNLKKNYCRNPDRRLRP----- 243  
 QY 187 GWTYFESRGVPSFTRVQPMILVGFFASFVMEVNPVSTMCIDQCTSPPPEQCNFVC 241  
 Db 244 -W-----CFTTDPN----KRWELCDIP-----RCTTPPSSGPTYOC 275  
 SQ

RESULT 15  
 AAV02100  
 ID AAV02100 Standard; protein; 566 AA.  
 XX  
 AC AAV02100;  
 XX  
 DT 16-JUL-1999 (first entry)  
 XX  
 DE A multifunctional protein of the invention.  
 XX  
 KW Angiostatin; endostatin; interferon; thrombospondin;  
 KW anti-interferon-inducible protein; Platelet Factor 4; anti-angiogenic;  
 KW diabetic retinopathy; multifunctional protein; angiogenic-mediated disease; cancer;  
 KW tumor cell production.  
 OS Synthetic.  
 OS Homo sapiens.  
 PN W09916889-A1.

Search completed: March 31, 2005, 02:03:03  
 Job time : 177 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.

Om protein - protein search, using sw model.

Run on: March 31, 2005, 01:57:45 ; Search time 43 Seconds

Sequence: 1 BQKILVGFAREVVSAHSVHR.....; (without alignments) 434.006 Million cell updates/sec

Title: US-10-771-708-11  
Perfect score: 1354  
Sequence: 1 BQKILVGFAREVVSAHSVHR.....; PPPETCQNFFVCKSVMMYNN 250

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqB, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Post-processing: Minimum DB seq length: 0  
Maximum Match 0%  
Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/1aa/POETUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score % Match Length DB ID Description

ALIGNMENTS

RESULT 1  
US 09-270-767-32874  
; Sequence 32874, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
; FILE REFERENCE: File Reference: 726-091  
; CURRENT APPLICATION NUMBER: US/09-270-767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO: 32874  
; LENGTH: 342  
; TYPE: PR  
; ORGANISM: *Drosophila melanogaster*  
; US 09-270-767-32874

Query Match 8.6%; Score 117; DB 4; Length 342;  
Best Local Similarity/23.6%; Pred. No. 0.00023; Mismatches 98; Indels 76; Gaps 15;  
Matches 64; Conservative 33; Mismatches 98; Indels 76; Gaps 15;

QY 3 KILVGFAREVVSAHSVHR.....;VHCLSLCNAEFTFGFECESVWVYVPAECL- 50  
Db 36 EITNG--VLSVAPSKMLDTLPGTMLTCAQON---NIFCSAVNY--EGLCVN 85  
QY 51 -NTEDRLDFDPLVDFDEBHDITVILUDNNCAG--CECHWRFDFNPKTSGLNDQQFAIAAC 106  
Db 85 KITADKLPG-SLSRSQFPVFTIVAQKSCIGVRFSKAWCIDR----- 126  
QY 107 YAPVTVQVAVERQLSVDLDHAFEGBLSECBRCLTORLRLSFTANDENCKSEMYSNLIRS 166  
Db 127 -----VQGYRILPEHVKSSTVLSRDCBLIC---LGBTEFTRSRANSYRHSCL 171  
QY 167 CVLSD-ERSRPLGRANLAEPVQWVTFESRGV--PS---FTRIPQMLVUGFASTVMENTP 219  
Db 172 CEISDMDRATLSAGGSVPIYDGAYLENCAEFSKLFCEFRKSQKILKTVDS-VHQDN 230  
QY 220 SVMCLDQCTSPPPETCQNFFVCKSVMMYNN 250  
Db 231 TIDSCRDCLNLSP----YRCHS--YDND 253

RESULT 2  
US-08-931-761A-13

Patent No. 520340  
Sequence 13, Application US/08991761A  
; Patent No. 6576609  
; GENERAL INFORMATION:  
; APPLICANT: Soff, Gerald  
; APPLICANT: Gateley, Stephen

27 7.3 812 1 US-08-326-785-1  
810 6 520340-8  
22 101 7.5 810 1 US-08-147-000B-29  
23 101 7.5 810 3 US-08-086-514-1  
24 101 7.5 810 4 US-09-192-012-5  
19 101 7.5 810 4 US-09-403-736-1  
20 101 7.5 810 4 US-08-924-287A-1  
16 101 7.5 810 1 US-07-854-603-2  
17 101 7.5 810 1 US-08-147-000B-29  
18 101 7.5 810 3 US-08-086-514-1  
19 101 7.5 810 4 US-09-192-012-5  
20 101 7.5 810 4 US-03-701-265-1  
22 101 7.5 810 6 520340-8  
23 101 7.5 810 520340-8  
24 101 7.5 814 1 US-08-750-711-1  
25 99 7.3 812 1 US-08-248-629A-1  
26 99 7.3 812 1 US-08-451-932-1  
27 99 7.3 812 1 US-08-452-260-1

APPLICANT: Twardowski, Przemyslaw  
 TITLE OF INVENTION: "Methods and Compositions for Generating  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sheridan Ross P.C.  
 STREET: 1700 Lincoln St., Suite 3500  
 CITY: Denver  
 STATE: CO  
 COUNTRY: USA  
 ZIP: 80203  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/991,761A  
 FILING DATE:  
 CLASSIFICATION: 1642  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Crook, Wanneill M.  
 REGISTRATION NUMBER: 31,071  
 REFERENCE/DOCKET NUMBER: 3501-16-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 863-9700  
 FAX: (303) 863-0223  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQENCE CHARACTERISTICS:  
 LENGTH: 790 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-991-761A-13

Query Match 8.6%; Score 116; DB 4; Length 790;  
 Best Local Similarity 19.5%; Pred. No. 0.00098; Matches 55; Conservative 43; Mismatches 100; Indels 84;  
 Matches 55; Conservative 43; Mismatches 100; Indels 84;

Qy	5	LVGFAREVVSADSVRHCLASCLNAFDITFGFECESVMYFVDAECLIMTEDRIL
Dy	14	LEFSIRKQVAAKSVEBCAKC-EAET-NFICARQHQSKDQCVWAENSK
Qy	65	EHDFTV-----YVLDNNCAGBCHWHDMPKTSQGLINDQOQFATAQCQAYPVW
Dy	68	RMRDVFLFEKRIVLSECKTGNGKNGRGTISKTKSGVICOKWSVSSPHIPKSYE
Qy	120	RQ-----LSDELDHFSGLESRCEELCQ-----RLSVA
Dy	128	LEENYCRNPNDNEKGCPWCYTTDPBTREFDYCIDIPECEDCMHCSGEGHVEGKISK
Qy	156	KS-----FMSNITRS-CVLSDRSRPPLGRANLAEPWTYFKE
Dy	188	QSGNSQSPHAGYIPLSPKPNKNIKMYCRNPDRCPRP-----W-----
Qy	200	TRVQMLLVGFASPVMEVNPVSVTMOLDQTSPPPETGONFVC 241
Dy	228	TTPDN-----KRWEFCOIP-----RCTTPPTSGPQYQC 256

RESULT 3  
 US-09-270-767-33129  
 ; Sequence 33129, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
 ; FILE REFERENCE: File Reference: 7326-054  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0





COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/643,219  
 FILING DATE: 06-MAY-1996  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Casuto, Diane  
 REGISTRATION NUMBER: 40,943  
 REFERENCE/DOCKET NUMBER: 5940.US.PI  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 847-938-3137  
 TELEFAX: 847-938-2623  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 791 amino acids  
 MOLECULE TYPE:  
 TOPOLOGY: amino acid  
 TYPE: linear  
 MOLECULE TYPE:  
 DESCRIPTION: protein

US-08-643-219-1

Query Match 7.5%: Score 101; DB 1; Length 791;  
 Best Local Similarity 18.0%; Pred. No. 0.045; Mismatches 90; Indels 110; Gaps 13;  
 Matches 53; Conservative 42; MisMatches 90; Indels 110; Gaps 13;

QY 5 LVGFAREVVASDVHRCVLSACLNADTGFGECESSVMYPPDAECLNTEDR---LDRP 59  
 Db 14 LFSVTKKQGAGSIEECAKCEEDEE--FTCRAQHYSKEQQVIMANRKKSIIRR 70  
 QY 60 DLFVDEHEHTVILYLDNNCAGCECHWHPDKPFTSGILNDQFAIAQCYAPVYQVAVEG 119  
 Db 71 DVLFEKK---VYLSCECKTGNGKNGYRGTMSKTKNGITCQKWSST---SPH----- 114  
 QY 120 RQLSDELDHSFEGLE-----LSECRILCTQ----- 144  
 Db 115 RPRFSPATHPSEGLEBNENYCRNPNDPQGPWCYTDPBKRYDYCILECEBECMCSGENY 174  
 QY 145 --RLSVTANDFNCKS-----FMYSLTRSCVLSDERSRPLGRANLAEP 186  
 Db 175 DGKISKTMGSLCQWDSDQSPHANGYIPLSPKPNKLNKGKNCRNPDRELRP----- 224  
 QY 187 GWTYFESRGVPSTRVQMLLVGFASFVMEVNSVTMCLDQCTSPPPERGQNFC 241  
 Db 225 -W-----CFTDPN----KRWELCDIP-----RCTTPPSSGPTYQC 256

RESULT 10

US-09-131-995-1

SEQUENCE 1, Application US/09131995

PATENT NO. 598184

GENERAL INFORMATION:

APPLICANT: Davidson, Donald J.

TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES

TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS

NUMBER OF INVENTIONS: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/131,995

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Casuto, Diane

REGISTRATION NUMBER: 40,943

REFERENCE/DOCKET NUMBER: 5940.US.PI

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847-938-3137

TELEFAX: 847-938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 791 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE:

DESCRIPTION: protein

US-09-131-995-1

Query Match 7.5%: Score 101; DB 2; Length 791;  
 Best Local Similarity 18.0%; Pred. No. 0.045; Mismatches 90; Indels 110; Gaps 13;  
 Matches 53; Conservative 42; MisMatches 90; Indels 110; Gaps 13;
QY 5 LVGFAREVVASDVHRCVLSACLNADTGFGECESSVMYPPDAECLNTEDR---LDRP 59  
 Db 14 LFSVTKKQGAGSIEECAKCEEDEE--FTCRAQHYSKEQQVIMANRKKSIIRR 70  
 QY 60 DLFVDEHEHTVILYLDNNCAGCECHWHPDKPFTSGILNDQFAIAQCYAPVYQVAVEG 119  
 Db 71 DVLFEKK---VYLSCECKTGNGKNGYRGTMSKTKNGITCQKWSST---SPH----- 114  
 QY 120 RQLSDELDHSFEGLE-----LSECRILCTQ----- 144  
 Db 115 RPRFSPATHPSEGLEBNENYCRNPNDPQGPWCYTDPBKRYDYCILECEBECMCSGENY 174  
 QY 145 --RLSVTANDFNCKS-----FMYSLTRSCVLSDERSRPLGRANLAEP 186  
 Db 175 DGKISKTMGSLCQWDSDQSPHANGYIPLSPKPNKLNKGKNCRNPDRELRP----- 224  
 QY 187 GWTYFESRGVPSTRVQMLLVGFASFVMEVNSVTMCLDQCTSPPPERGQNFC 241  
 Db 225 -W-----CFTDPN----KRWELCDIP-----RCTTPPSSGPTYQC 256

RESULT 11

US-08-832-087B-1

SEQUENCE 1, Application US/08832087B

PATENT NO. 598184

GENERAL INFORMATION:

APPLICANT: Davidson, Donald J.

TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES

TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

US-08-832-087B-1

APPLICATION NUMBER: US/08/851,350  
 CURRENT APPLICATION DATA:  
 FILING DATE: 05-MAY-1997  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/643,219  
 FILING DATE: 06-MAY-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Casullo, Diane  
 REGISTRATION NUMBER: 40,943  
 REFERENCE/DOCKET NUMBER: 5940.US.P1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 847-938-3137  
 TELEX: 847-938-2623  
 TELER: INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 791 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE:  
 DESCRIPTION: protein  
 US-08-832-087B-1

Query Match 7.5%; Score 101; DB 2; Length 791;  
 Best Local Similarity 18.0%; Pred. No. 0 045; Mismatches 90; Indels 110; Gaps 13;  
 Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

Qy 5 LVGFAREVVSANSVHRCISACAINA[ADTFPGFECESWVYYPVDAECLNTEDR----LDRP 59  
 Db 14 LFSVTKKGAGSIEECAKCKEDEE--FTCRAQYHSKEQQCVIMAENRKSSIIIRMR 70  
 Qy 60 DLVFDDEHDIVLNDNCAGCCHWHFDNEFKSGILNDQFRAQCYAPVYAVEG 119  
 Db 71 DVLFLERKK--VYLSCKTGNGKNGYRGTMSKTRNGITCOKNST---SPH----- 114  
 Qy 120 RQLSDELDHSFEGLE-----LSECEELCTQ----- 144  
 Db 115 RPRFSPATHPSGSLBENLYCRNPDPQGPWCYTDPERKRYDYLCEECMHCSGENY 174  
 Qy 145 -RLSVTANDFNCKS-----FMYNSLITRS-CVLSDERSRPLGRANIAEV 186  
 Db 175 DGKISKTMGSLCQAMDSQSPHANGYIPSKFPNKLKQVNCNPDRLRP----- 224  
 Qy 187 GWTYFESRGVPSFTRVPOMLVGFASFWNTVPSVTMCLQDTSPPETGONFVC 241  
 Db 225 -W-----CFTDPN-----KRWELCDP-----RCTIPPPSSGPTYQC 256

RESULT 12  
 US-08-851-350-1  
 Sequence 1, Application US/08851350  
 Patent No. 6057122

GENERAL INFORMATION:  
 APPLICANT: Abbott Laboratories  
 TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES, POLYNUCLEOTIDES ENCODING SAME, AND METHODS  
 TITLE OF INVENTION: FOR INHIBITING ANGIOGENESIS  
 NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Abbott Laboratories  
 STREET: 100 Abbott Park Road  
 CITY: Abbott Park  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60064-3500

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 2.0

OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/132,154  
 FILING DATE:  
 CLASSIFICATION:

APPLICATION NUMBER: US/08/851,350  
 CURRENT APPLICATION DATA:  
 FILING DATE: 05-MAY-1997  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Casullo, Diane  
 REGISTRATION NUMBER: 40,943  
 REFERENCE/DOCKET NUMBER: 5940.US.P2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 847-938-3137  
 TELEX: 847-938-2623  
 TELER: INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 791 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE:  
 DESCRIPTION: protein  
 US-08-851-350-1

Query Match 7.5%; Score 101; DB 3; Length 791;  
 Best Local Similarity 18.0%; Pred. No. 0.05; Mismatches 90; Indels 110; Gaps 13;  
 Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

Qy 5 LVGFAREVVSANSVHRCISACAINA[ADTFPGFECESWVYYPVDAECLNTEDR----LDRP 59  
 Db 14 LFSVTKKGAGSIEECAKCKEDEE--FTCRAQYHSKEQQCVIMAENRKSSIIIRMR 70  
 Qy 60 DLVFDDEHDIVLNDNCAGCCHWHFDNEFKSGILNDQFRAQCYAPVYAVEG 119  
 Db 71 DVLFLERKK--VYLSCKTGNGKNGYRGTMSKTRNGITCOKNST---SPH----- 114  
 Qy 120 RQLSDELDHSFEGLE-----LSECEELCTQ----- 144  
 Db 115 RPRFSPATHPSGSLBENLYCRNPDPQGPWCYTDPERKRYDYLCEECMHCSGENY 174  
 Qy 145 -RLSVTANDFNCKS-----FMYNSLITRS-CVLSDERSRPLGRANIAEV 186  
 Db 175 DGKISKTMGSLCQAMDSQSPHANGYIPSKFPNKLKQVNCNPDRLRP----- 224  
 Qy 187 GWTYFESRGVPSFTRVPOMLVGFASFWNTVPSVTMCLQDTSPPETGONFVC 241  
 Db 225 -W-----CFTDPN-----KRWELCDP-----RCTIPPPSSGPTYQC 256

RESULT 13  
 US-09-132-154-1  
 Sequence 1, Application US/09132154  
 Patent No. 6251867

GENERAL INFORMATION:  
 APPLICANT: Davidson, Donald J.  
 TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Abbott Laboratories  
 STREET: 100 Abbott Park Road  
 CITY: Abbott Park  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60064

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/132,154  
 FILING DATE:  
 CLASSIFICATION:



QY	5	LVGKAREVNSADSVTIRCLSACTINANRTPGFCESVMMYPVDRACILTEDR-----LDRP 59
Db	14	LFSVTKQOLGAGSISBAAKCEEDEEF---FTCRAFOHFSKSEQQVIMAENRKSIIIRMR 70
QY	60	DLFVDEHEDTVIYLDNNCAGCECHHNFDNFKITSGLINDQQFAIAACQYAPVYQYAVEG 119
Db	71	DVULERKK---VYLSECKTGKNGKNTGTMCKTNGKIGTICQKNSST-----SPH----- 114
QY	120	ROLSELDHSFEGLE-----LSBCEELCTQ----- 144
Db	115	RPRFSSPATHPSEGLENYCNPDPDNPOGPWCYTDPKRYDCCDILECEEWMHCSGENY 174
QY	145	--RISVTAENDFNCKS-----PMYSNUTRS-CVLSRDRSRPLGRANLAEV 186
Db	175	DGKISKRTMMSGLECQAWDSQSPHAGYIPTSKFPNKNLKKYCRNPDRBLRP----- 224
QY	187	GWTYFESRGVPSFRVUPQMLLVGFASFVMENVPSTVWCLDORTSPPETGQNFC 241
Db	225	-W-----CFTDPN-----KRWELCDP-----RCTTPPSGGPYQC 256

Search completed: March 31, 2005, 02:07:44  
Job time : 44 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2005, 02:00:10 ; Search time 140 Seconds  
(without alignments)  
591.252 Million cell updates/sec

Title: US-10-771-708-11  
Perfect score: 134  
Sequence: 1 BQKILVGFAREVVSADSVHR..... PPPETGQNFFVCKSVMYYNE 250

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext: 0.5

Searched: 1407402 seqs, 331100923 residues  
Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database : Published Applications AA:  
1: /cgnd\_5/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgnd\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgnd\_6/ptodata/2/pubpaa/US06\_PUB.pep:\*

4: /cgnd\_6/ptodata/2/pubpaa/US05\_PUBCOMB.pep:\*

5: /cgnd\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgnd\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

7: /cgnd\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

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9: /cgnd\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

10: /cgnd\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgnd\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgnd\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgnd\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

14: /cgnd\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*

15: /cgnd\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*

16: /cgnd\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep:\*

17: /cgnd\_6/ptodata/2/pubpaa/US10F\_NEW\_PUB.pep:\*

18: /cgnd\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*

19: /cgnd\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

20: /cgnd\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1  
US-09-825-751A-70  
; Sequence 70, Application US/09925751A  
; Publication No. US20030065140A1  
; GENERAL INFORMATION:  
; APPLICANT: Curagen Corporation  
; APPLICANT: Vernet, Corine A.M.  
; APPLICANT: Fernandes, Elma R.  
; APPLICANT: Taurier, Raymond J  
; APPLICANT: Quinn, Kerry E  
; APPLICANT: Spretek, Kimberly A  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Herman, John L

CURRENT APPLICATION NUMBER: US/09/825,751A

PRIOR APPLICATION NUMBER: 60/194,314

PRIOR FILING DATE: 2000-04-30  
FILE REFERENCE: 15966-750

TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same

PRIOR FILING DATE: 2000-08-16  
NUMBER OF SEQ ID NOS: 85

SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 70  
; LENGTH: 790

; TYPE: PRT  
; ORGANISM: Sub scrofa

US-09-825-751A-70  
Query Match 8.6% Score 116, DB 10, Length 790;  
Best Local Similarity 19.5%, Pred. No. 0.0064, Gaps 84, Gaps 12;  
Matches 55; Conservative 43; Mismatches 100; Indels 84;

Qy 5 LVGFAREVVSADSVHRCLACLNADPFTGPFECESVMYVPAECLNLNEDRLDRPDLFD 64

Db 14 LFLSLRKQVAARSVECAAKC--EAET-NPICRAFQYHNSKDQQCVWMAENSKTSP--IA 67

QY 65 EHEDTV----IYLDNNCAGCSECHWFDNFKPSGLNDQQFAIAQCYAPIVTOVAVEG 119

Db 68 RMRDVLVLFERKTRIVLSECKTGNGNYRGTTSKKGWVCKWMSVSPKPLAG 127

QY 120 RQ----LSDLDHSFEGLELSECEBLCTQ----RLSTVANDFNC 155

Db 128 LSENYCRNPNDNBKGPMCYTTPETRFDYCDIPCECDKMHGSGHRYBGKVSSTMMSGIEC 187

QY 156 KS----FMYSULTRS-CVLSRSRSLPGRANLAEVPGWTFFESRCVPSF 199

Db 188 QWGSOSPHAH3YLPSKFPNPKLNKMYCRNPDPGEPRP----W----CF 227

QY 200 TRVPQMLLGVFAASFVMEVNPVSMCLDOCTSPPPETGONFVC 241

Db 228 TTDPN----KRWEFCDIP----RCTTPPSSGPTYOC 256

RESULT 2

US-09-825-751A-71

; Sequence 71, Application US/09825751A

; Publication No. US20030065140A1

; GENERAL INFORMATION:

; APPLICANT: CuraGen Corporation

; APPLICANT: Vernet, Coirine A.M.

; APPLICANT: Fernandes, Elma R.

; APPLICANT: Taurier, Raymond J

; APPLICANT: Quinn, Kerri E

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Rastelli, Luca

; APPLICANT: Herman, John L

; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 15966-550

; CURRENT APPLICATION NUMBER: US/09/825,751A

; CURRENT FILING DATE: 2001-04-30

; PRIOR APPLICATION NUMBER: 60/194,314

; PRIOR FILING DATE: 2000-04-03

; PRIOR APPLICATION NUMBER: 60/225,693

; PRIOR FILING DATE: 2000-08-16

; NUMBER OF SEQ ID NOS: 85

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 71

; LENGTH: 812

; TYPE: PRT

; ORGANISM: Bos taurus

; US-09-825-751A-71

Query Match 7.8%; Score 105; DB 10; Length 812;

, Matches 55; Conservative 42; Mismatches 83; Indels 120; Gaps 17;

, Best Local Similarity 18.3%; Pred. No. 0 096;

, Title of Invention: Novel Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 15966-550

; CURRENT APPLICATION NUMBER: US/09/825,751A

; CURRENT FILING DATE: 2001-04-30

; PRIOR APPLICATION NUMBER: 60/194,314

; PRIOR FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 85

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 71

; LENGTH: 812

; TYPE: PRT

; ORGANISM: Bos taurus

US-10-741-601-413

; Sequence 413, Application US/10741601

; Publication No. US20040166519A1

; GENERAL INFORMATION:

; APPLICANT: Cargill, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: C1001500

; CURRENT APPLICATION NUMBER: US/10/741,601

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 26415

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 413

; LENGTH: 567

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-741-601-413

Query Match 7.5%; Score 101; DB 16; Length 567;

; Best Local Similarity 18.0%; Pred. No. 0 16; Mismatches 90; Indels 110; Gaps 13;

; Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

; GENERAL INFORMATION:

; APPLICANT: Cao, Yihai

; TITLE OF INVENTION: Materials and methods relating to endothelial cell growth

; TITLE OF INVENTION: Inhibitor

; FILE REFERENCE: Mewburn

; CURRENT APPLICATION NUMBER: US/09/946,893

; CURRENT FILING DATE: 2001-09-05

; PRIOR APPLICATION NUMBER: US 60/230,893

; PRIOR FILING DATE: 2000-09-05

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 5

; LENGTH: 569

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: Other Information: Description of Artificial Sequence: Angioquiescin

; US-09-946-893-5

Query Match 7.5%; Score 101; DB 9; Length 569;

; Best Local Similarity 18.0%; Pred. No. 0 16; Mismatches 90; Indels 110; Gaps 13;

; Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

; GENERAL INFORMATION:

; APPLICANT: Leng, Ming

; TITLE OF INVENTION: Methods of detection and uses thereof

; FILE REFERENCE: C1001500

; CURRENT APPLICATION NUMBER: US/10/741,601

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 26415

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 413

; LENGTH: 569

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: Other Information: Description of Artificial Sequence: Angioquiescin

; US-09-946-893-5

Query Match 7.5%; Score 101; DB 9; Length 569;

; Best Local Similarity 18.0%; Pred. No. 0 16; Mismatches 90; Indels 110; Gaps 13;

; Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

; GENERAL INFORMATION:

; APPLICANT: Leng, Ming

; TITLE OF INVENTION: Methods of detection and uses thereof

; FILE REFERENCE: C1001500

; CURRENT APPLICATION NUMBER: US/10/741,601

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 26415

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 413

; LENGTH: 569

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: Other Information: Description of Artificial Sequence: Angioquiescin

; US-09-946-893-5

Query Match 7.5%; Score 101; DB 9; Length 569;

; Best Local Similarity 18.0%; Pred. No. 0 16; Mismatches 90; Indels 110; Gaps 13;

; Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

; GENERAL INFORMATION:

; APPLICANT: Leng, Ming

; TITLE OF INVENTION: Methods of detection and uses thereof

; FILE REFERENCE: C1001500

; CURRENT APPLICATION NUMBER: US/10/741,601

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 26415

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 413

; LENGTH: 569

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: Other Information: Description of Artificial Sequence: Angioquiescin

; US-09-946-893-5

Query Match 7.5%; Score 101; DB 9; Length 569;

; Best Local Similarity 18.0%; Pred. No. 0 16; Mismatches 90; Indels 110; Gaps 13;

; Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

; GENERAL INFORMATION:

; APPLICANT: Leng, Ming

; TITLE OF INVENTION: Methods of detection and uses thereof

; FILE REFERENCE: C1001500

; CURRENT APPLICATION NUMBER: US/10/741,601

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 26415

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 413

; LENGTH: 569

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: Other Information: Description of Artificial Sequence: Angioquiescin

; US-09-946-893-5



QY 60 DLFVDEHEHDTVYILDNNCAGCCECHWMFDNKTSGLINDQQFAIAACQYAPVTVQVAVEG 119  
 CURRENT APPLICATION NUMBER: US 10/360,101  
 CURRENT FILING DATE: 2003-02-07  
 PRIORITY APPLICATION NUMBER: EP 02077050.8  
 PRIORITY FILING DATE: 2002-05-24  
 NUMBER OF SEQ ID NOS: 309  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO: 257  
 LENGTH: 791  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: sequence of plasminogen

Db 71 DVLFEKK--VYLSECKTGKNGVYRGTMSKTKNGITCQKNSST---SPH----- 114  
 120 RQLSDELDHSFPEGLE-----LSECBELCTQ----- 144  
 115 RPRFSPATHPSGLEENYCRNPDNDPQGPWCYTDPKRYDYLDCILECEECMHCSGENY 174  
 QY 145 -RLSVPANDFCKS-----FMYSLNLTRS-CVLSDDRSRPIGRANLAEPV 186  
 Db 175 DGKISKTMMSGLEQWDQSOPHAGYIPSKFPNKNLKKNYCRNPDRLRP----- 224  
 QY 187 GWTYFESRGVPSFTRVQMLLVGFASFVMENTPSVTMCLDQCTSPPETQNFVC 241  
 Db 225 -W-----CFTTDPN-----KRWELCDIP-----RCTTPPPSSGPTYQC 256  
 ; US-10-304-287-1

RESULT 8

Query Match 7.5%; Score 101; DB 14; Length 791;  
 Best Local Similarity 18.0%; Pred. No. 0.24; Mismatches 90; Indels 110; Gaps 13;  
 Matches 53; Conservative 42; MisMatches 90; Indels 110; Gaps 13;  
 Sequence 1, Application US/10304287  
 Publication No. US20030083234A1  
 GENERAL INFORMATION:  
 APPLICANT: Walzman, David M.  
 TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor  
 FILE REFERENCE: ME02-001  
 CURRENT APPLICATION NUMBER: US/10/304,287  
 CURRENT FILING DATE: 2002-11-28  
 PRIOR APPLICATION NUMBER: US 60/333,866  
 PRIOR FILING DATE: 2001-11-28  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: Microsoft Word  
 SEQ ID NO: 1  
 LENGTH: 791  
 TYPE: PRT  
 ORGANISM: mammalian  
 ; US-10-304-287-1

Query Match 7.5%; Score 101; DB 15; Length 791;  
 Best Local Similarity 18.0%; Pred. No. 0.24; Mismatches 90; Indels 110; Gaps 13;  
 Matches 53; Conservative 42; MisMatches 90; Indels 110; Gaps 13;  
 Sequence 1, Application US/10304287  
 Publication No. US20030083234A1  
 GENERAL INFORMATION:  
 APPLICANT: Walzman, David M.  
 TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor  
 FILE REFERENCE: ME02-001  
 CURRENT APPLICATION NUMBER: US/10/304,287  
 CURRENT FILING DATE: 2002-11-28  
 PRIOR APPLICATION NUMBER: US 60/333,866  
 PRIOR FILING DATE: 2001-11-28  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: Microsoft Word  
 SEQ ID NO: 1  
 LENGTH: 791  
 TYPE: PRT  
 ORGANISM: mammalian  
 ; US-10-304-287-1

RESULT 9

Query Match 7.5%; Score 101; DB 16; Length 791;  
 Best Local Similarity 18.0%; Pred. No. 0.24; Mismatches 90; Indels 110; Gaps 13;  
 Matches 53; Conservative 42; MisMatches 90; Indels 110; Gaps 13;  
 Sequence 1, Application US/10360101  
 Publication No. US2004009550A1  
 GENERAL INFORMATION:  
 APPLICANT: Moll, Gert N.  
 APPLICANT: Deenhouws, Cornelis J.  
 TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way  
 FILE REFERENCE: 2183-5673

QY 5 LVGFAREVVSAVSVRCLSACINAADFPGFECESVMMYVPUAECILNTEDR----LDRP 59  
 CURRENT APPLICATION NUMBER: US 10/778-423-1  
 CURRENT FILING DATE: 2003-09-29  
 NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 1  
 LENGTH: 791  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 ; US-10-778-423-1

Query Match 7.5%; Score 101; DB 16; Length 791;  
 Best Local Similarity 18.0%; Pred. No. 0.24; Mismatches 90; Indels 110; Gaps 13;  
 Matches 53; Conservative 42; MisMatches 90; Indels 110; Gaps 13;  
 Sequence 1, Application US/10360101  
 Publication No. US2004009550A1  
 GENERAL INFORMATION:  
 APPLICANT: Moll, Gert N.  
 APPLICANT: Deenhouws, Cornelis J.  
 TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way  
 FILE REFERENCE: 2183-5673

QY 5 LVGFAREVVSAVSVRCLSACINAADFPGFECESVMMYVPUAECILNTEDR----LDRP 59  
 Db 14 LFSVTKKQLGAGSIECAKCEEDEE--FTCRAFOYHSKQOCVIMAENRKSSIIIRMR 70  
 QY 60 DLFVDEHEHDTVYILDNNCAGCCECHWMFDNKTSGLINDQQFAIAACQYAPVTVQVAVEG 119  
 Db 71 DVLFEKK--VYLSECKTGKNGVYRGTMSKTKNGITCQKNSST---SPH----- 114  
 120 RQLSDELDHSFPEGLE-----LSECBELCTQ----- 144  
 115 RPRFSPATHPSGLEENYCRNPDNDPQGPWCYTDPKRYDYLDCILECEECMHCSGENY 174  
 QY 145 -RLSVPANDFCKS-----FMYSLNLTRS-CVLSDDRSRPIGRANLAEPV 186  
 Db 175 DGKISKTMMSGLEQWDQSOPHAGYIPSKFPNKNLKKNYCRNPDRLRP----- 224  
 QY 187 GWTYFESRGVPSFTRVQMLLVGFASFVMENTPSVTMCLDQCTSPPETQNFVC 241  
 Db 225 -W-----CFTTDPN-----KRWELCDIP-----RCTTPPPSSGPTYQC 256  
 ; US-10-778-423-1

RESULT 9

Query Match 7.5%; Score 101; DB 16; Length 791;  
 Best Local Similarity 18.0%; Pred. No. 0.24; Mismatches 90; Indels 110; Gaps 13;  
 Matches 53; Conservative 42; MisMatches 90; Indels 110; Gaps 13;  
 Sequence 1, Application US/10360101  
 Publication No. US2004009550A1  
 GENERAL INFORMATION:  
 APPLICANT: Moll, Gert N.  
 APPLICANT: Deenhouws, Cornelis J.  
 TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way  
 FILE REFERENCE: 2183-5673

QY 60 DLFVDEHEHDTVYILDNNCAGCCECHWMFDNKTSGLINDQQFAIAACQYAPVTVQVAVEG 119



RESULT 15  
US-10-237-144-1  
; Sequence 1, Application US/10237144



R;Matthews, P.  
submitted to the EMBL Data Library, January 1996  
A;Reference number: Z19495  
A;Accession: T21967  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-751 <WIL>  
A;Cross-references: UNIPROT:Q20167; EMBL:Z68342; PIDN:CAA92773.1; GSPDB:GN00022; CESP:F3  
A;Experimental source: clone F38E11  
C;Genetics:  
A;Gene: CESP:F38E11.4  
A;Map position: 4  
A;Introns: 23/1; 68/3; 116/1; 210/1; 284/1; 307/1; 359/3; 539/3; 622/2; 660/1; 695/2

Query Match 19.4%; Score 262; DB 2; Length 751;  
Best Local Similarity 27.4%; Pred. No. 5 7e-16;  
Matches 73; Conservative 37; Mismatches 98; Indels 58; Gaps 8;

Qy 2 QKILVGFAREKVSADSVERCISACLNADTFEFRECEVMMYVVDACILNTEDRDRPDL 61  
Db 131 QSLILGHAMKVLIVDGLSDCLSCALSORSYLFLCKSAYVYETGECIMRNDRKFLYPL 190

Qy 62 FDEDEHEPTVYLDDNGAGC-----HWHDNFNFKTSGLNDQQFIAACQYAPVQY 114  
Db 191 FKNILDTLVDFENNGADVSCKPPELTW----- 220

Qy 115 VAVEGROLSDLDHSFEGLELSCEECLTQRISVANDFNCKSFMSNLTRSCVSDERS 174  
Db 221 VTEEYVLDSESDVIVESSDAGCNCQLC-QNNKIGEENPCKAFAVNSKOECHTAESS 279

Qy 175 ---RPLGRANLAEVPGWYFPRSGRV-----SPTRVQMLLVGFASFMENVPST 222  
Db 280 YTGKKGDKRKNLAPLNSGBYFFEKVCLPNTNQCLIEASPELVARMMT--SAYKTTISALQH 337

Qy 223 MLDQCTSPPPPTGQNIVCKSYMMY 248  
Db 338 ECLSQCKNDGAR-----CSSAIVFY 357

RESULT 3

T22486 hypothetical protein F52B11.3 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T22486  
R;Matthews, L.  
A;Reference number: 219569  
A;Accession: T22486  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Residues: 1-41 <WIL>  
A;Cross-references: UNIPROT:Q9XUE5; EMBL:Z82268; PIDN:CAB05199.1; GSPDB:GN00022; CESP:F52B11.1  
A;Experimental source: clone F52B11  
C;Genetics:  
A;Gene: CESP:F52B11.3  
A;Map position: 4  
A;Introns: 48/1; 298/1; 341/3; 690/2

Query Match 12.4%; Score 168; DB 2; Length 741;  
Best Local Similarity 22.5%; Pred. No. 2.5e-07; Indels 124; Gaps 15;  
Matches 76; Conservative 38; Mismatches 100; Indels 124; Gaps 15;

Qy 5 LVGFARVEVSAASVHRCILSACLNAAFDTGECESVMYVYDAACTINTEDRDRPLFVD 64  
Db 137 LEGFVFKSVTENREHCLSACKKE--FVCKSIVFHYTSLCLSIVEDKRSKE---- 188

Qy 65 EH--EDTVIYIDNNGAG-----C--EC 82  
Db 189 THVRNSEKIDYIDNCLSLRQNRGPGSGGNLVFVKTNFERYDHTQSVAQESYCLQK 248

Qy 83 HWHEDFDKFTSCLN-----DQ-----FAIAQCYAPVQY 114

Db 249 LDSLNTFRCRSVEFPNPKEKNCIVSDDTFSPRADQPGQVVKOYKYPEICVAADLSSSTCROQ 308  
Qy 115 VAVE--GROSLDHSFEGLELSCEECLTQRISVANDFNCKSFMSNLTRSCVSD 171  
Db 309 AAERFTGSSIEGEVWVAAQCVTSDCISLCFQNL----NCKSINTDRTASSCFI-- 359

Qy 172 ERSRPLIGR--ANLAEVPGWYFESRGVPSF-----TRPQMLLVGFPA-- 211  
Db 360 ---YAVGRQDANIKANPMSMDOYEFCESPRGGMALCTNFGIRFIVNTKPYTGIAABR 416

Qy 212 ---SFVMMENPSVNLQDCTSPPPETGQNFVCKSV 245  
Db 417 FSTCSQVWENAKQISI-----TFPPPTVSSD--CGTVI 447

RESULT 4

G89459 protein C52B11.1 [imported] - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Nov-2001  
C;Accession: G89459  
R;anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology  
A;Residues: A75000; PMID:9905613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/c\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans  
A;Accession: G89459  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-282 <STO>  
A;Cross-references: GB:chr\_X; PIDN:AAA82467.1; PID:g1086885; GSPDB:GN00028; CESP:C52B11.1  
A;Genetics:  
A;Map position: X

Qy 112 TQWAVEGROLSDLDHSFEGLELSCEECLTQRISVANDFNCKSFMSNLTRSCVLSD 171  
Db 31 THFVTDNALSQADPIVVKATSEECLTQRISVANDFNCKSFMSNLTRSCVLSD 171

Qy 172 ERSRPLIGRANLAEVPGWTFE-----SRGV-----SPTRVQMLLVGFASFMENVPST 221  
Db 91 EKSAPVGSQIENSVGKRYFKEKILSHNIPQOCQTOFRVQDSVLVGA-VNMTLDSI 149

Qy 222 TMCLDQCTSPPPPTGQNFVCKSYMMY 250  
Db 150 ESCAAQCV-----QEADCKSAMVYED 171

RESULT 5

T32444 hypothetical protein H42K12.3 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T32444; T35821  
R;Maggi, L.; Harper, M.;  
submitted to the EMBL Data Library, September 1997  
A;description: The sequence of *C. elegans* cosmid H42K12.  
A;description: The sequence of *C. elegans* cosmid H42K12.  
A;Accession: T32444  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-522 <MAG>  
A;Cross-references: UNIPROT:O17347; EMBL:AE026207; PIDN:AAA71266.1; GSPDB:GN00028; CESP:F52B11.1  
A;Experimental source: strain Bristol N2; clone H42K12  
R;Martin, J.  
submitted to the EMBL Data Library, November 1995  
A;description: The sequence of *C. elegans* cosmid C52B11.  
A;reference number: Z18411

A;Accession: T15821  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-351 <WIL>  
 A;Cross-references: UNIPROT:Q21782; EMBL:267756; PIDN:CAA91764\_1; GSPDB:GN00028; CESP:R07A4  
 C;Genetics:  
 A;Gene: CESP:H42K12.3; CESP:C52B11.1  
 A;Map position: X  
 A;Introns: 24/1; 65/3; 117/1; 163/3; 208/1; 281/1; 381/3; 430/1; 481/3  
 Query Match 11.8%; Score 160; DB 2; Length 522;  
 Best Local Similarity 28.9%; Pred. No. 8.7e-07; Mismatches 71; Indels 18; Gaps 4;  
 Matches 43; Conservative 17; Mismatches 71; Indels 18; Gaps 4;  
 Qy 112 TQYVAVEGROLSDLDHSFEGGLELSECEELCTQRLSUTANDDFNCFSFPMYSNLRSCLVLSD 171  
 Db 31 THFVFDNLSQASDPIVVKATSBRECLACTKNDKFRPVCVQFVTDHAAASCTIK 90  
 Qy 172 ERSRPLGRNLALAEVPGWTFFE---SRGVPP---SFTRVPPQMLVNGASFWMENVS 221  
 Db 91 EKASPAVGSAQIENSVGKRVFEKICLHSNIPQCAOTQFIRUDQSVLNGA-VNNLTDSDI 149  
 Qy 222 TMCUQOCTSPRPTGCONFVCKSVMYNE 250  
 Db 150 ESCAAQCV-----QEADCKSAMFYED 171

RESULT 6  
 T29557  
 hypothetical protein C16D9.1 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T29557  
 R;Gattting, S.; Le, T.T.  
 Submitted to the EMBL Data Library, July 1996  
 A;Description: The sequence of *C. elegans* cosmid C16D9.  
 A;Reference number: 220640  
 A;Accession: T29557  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-342 <BEN>  
 A;Cross-references: UNIPROT:Q22902; EMBL:U64058; PIDN:AAB18288\_1; GSPDB:GN00023; CESP:C1  
 A;Experimental source: Strain Bristol N2; Clone C16D9  
 A;Gene: CESP:C16D9.1  
 A;Map position: 5  
 A;Introns: 59/2; 316/3  
 Query Match 11.3%; Score 153.5; DB 2; Length 342;  
 Best Local Similarity 38.2%; Pred. No. 2.1e-06; Mismatches 29; Conservative 10; Indels 26; Gaps 2;  
 Matches 29; Conservative 10; Mismatches 26; Indels 3; Gaps 2;  
 Qy 3 KILVGFAREVV-SADSVHRLCLACINAFDFGFECEWMVYPPDRECLNTEDRDPDL 61  
 Db 121 KVLIGVQDQLRDRVATVNDQACQCSNSQTKYDICKSAMYKEDKECILASQSKADIPDL 180  
 Db 181 FID-DDKSIXLENS 194

RESULT 7  
 T23990  
 hypothetical protein R07M4.4 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T23990  
 R;Cottage, A.  
 submitted to the EMBL Data Library, November 1995  
 A;Reference number: 219827  
 A;Accession: T23990  
 A;Status: preliminary; translated from GB/EMBL/DBJ

RESULT 8  
 T28804  
 hypothetical protein H03E18.1 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T28804  
 R;Bentley, D.  
 submitted to the EMBL Data Library, August 1996  
 A;Description: The sequence of *C. elegans* cosmid H03E18.  
 A;Reference number: 220900  
 A;Accession: T28804  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-117 <BEN>  
 A;Cross-references: UNIPROT:Q94248; EMBL:UG7947; PIDN:AAB07557\_1; GSPDB:GN00028; CESP:H01  
 A;Experimental source: Strain Bristol N2; Clone H03E18  
 C;Genetics:  
 A;Gene: CESP:H03E18.1  
 A;Map position: X  
 A;Introns: 112/3; 217/1; 282/2; 304/1; 424/1; 461/2; 579/3; 615/2; 831/1; 999/2; 1088/1  
 Query Match 9.2%; Score 124.5; DB 2; Length 1127;  
 Best Local Similarity 22.3%; Pred. No. 0.0041; Mismatches 44; Conservative 37; Indels 41; Gaps 9;  
 Matches 44; Conservative 37; Mismatches 75; Indels 41; Gaps 9;  
 Qy 1 EOKTILGFREVV-SADSVHRLCLACINAFDFGFECEWMVYPPDRECLNTEDRDP 58  
 Db 433 DDHLKAVSGAGGLEHDMSSTRCQCMNCANSKTSRRFEPQCSATYHAEKICLNLDRNTK 492  
 Qy 59 PDLFVDEHED-TWYLDNNG-----AGCECHWHD-----NFKTSGIL 95  
 Db 493 SKLFFKQFDVNVVYVIGLACEVDETVKSGLSLATECREKVEATGEPKETSKKNGK 552  
 Qy 96 NDQOFAIAQACYAPVYVQAVEGROLSDLDHSFEGGLSISCECLCTORLSVTANDFNC 155  
 Db 553 SD-----DCYVE-LNDTV-LEGTAIAVE-----TAVTPEECKCAGHKLGYEE-C 596  
 Qy 155 KSFMYSNLRSCLVSD 172  
 Db 597 ASFLXYDDEKCLINKQ 613

RESULT 9  
 P1PG  
 Plasmin (EC 3.4.21.7) precursor - pig (fragment)  
 N;Alternate names: plaminogen  
 N;Contains: miniplasminogen

C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 07-Sep-1990 #sequence revision 01-Nov-1996 #text\_change 09-Jul-2004  
 C;Accession: S03733; S03737; A25834  
 R;Schaller, J.; Marti, T.; Roessel, S.J.; Kempfer, U.; Rickli, B.E.  
 Fibriolysis I, 91-102, 1987  
 A;Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the ca  
 A;Reference number: S03733  
 A;Accession: S03733  
 A;Molecule type: protein  
 A;Residues: 1-1560 <SCH>  
 A;Cross-references: UNIPROT:P06867  
 R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, B.E.; Lergier, W.; Manneberg, M.;  
 Eur. J. Biochem. 114, 465-470, 1981  
 A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, a  
 A;Reference number: S03735; MUID:81212097; PMID:7238497  
 A;Accession: S03737  
 A;Molecule type: protein  
 A;Residues: 1-57 <BRU>  
 R;Marti, T.; Schaller, J.; Rickli, B.E.  
 Eur. J. Biochem. 149, 278-285, 1985  
 A;Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.  
 A;Reference number: A25834; MUID:85203907; PMID:3846533  
 A;Accession: A25834  
 A;Molecule type: protein  
 A;Residues: 450-790 <MAR>  
 C;Function:  
 A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va  
 ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act  
 A;Pathway: fibrinolysis  
 C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology  
 C;Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine prote  
 P;1-790/Product: plasminogen #status predicted <PRO>  
 P;1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>  
 P;1-77/Domain: activation peptide #status predicted <ACT>  
 P;78-560/Domain: plasmin chain A #status predicted <ACT>  
 P;84-162/Domain: kringle homology <KR1>  
 P;166-243/Domain: kringle homology <KR2>  
 P;256-333/Domain: kringle homology <KR3>  
 P;358-435/Domain: kringle homology <KR4>  
 P;450-790/Product: miniplasminogen #status experimental <MIN>  
 P;461-540/Domain: kringle homology <KR5>  
 P;561-783/Domain: trypsin homology <TRY>  
 P;30-42, 84-162, 105-145, 133-157, 166-243, 169-297, 187-226, 215-238, 256-333, 277-316, 305  
 bonds; #status Predicted  
 P;602, 645, 740/Active site: His, Asp, Ser #status predicted

Query Match 8.6%; Score 116; DB 1; Length 790;  
 Best Local Similarity 19.3%; Pred. No. 0\_016; Indels 84; Gaps 12;  
 Matches 55; Conservative 43; Mismatches 100; Indels 84; Gaps 12;  
 QY 5 LIGFAREVVSADSHRCRCLASACINAADFDFGFECESSVMYVPUDEACTINTEDRLRDLFVD 64  
 Db 14 LFLSLRKQVAARSVECAAKC-EAET-NFICRAFOYHSKQDQCVMAENSKTSP--IA 67  
 QY 65 EHDFTV----YLDNNCAGCCHWIFDNFKSGILNDQDFAIAQCYAPVYQVAVEG 119  
 Db 68 RMRDVLVLFKRYLSECKTGNGKNYRGTTSKKSGVQICQKWSVSSPHIPKYSPEKPLAG 127  
 QY 120 RQ-----LSDLDHREGELSECELCTQ-----RLSNTANDFNC 155  
 Db 128 LHENYCRNPDNDKGPWCYTIDPTEFRDYCDPECDECCHMCSGERHEYEGKISKMSIEC 187  
 QY 156 KS-----FMSNLTRAS-CVLSDESPPLGRANLAEVPGWTVFESRGVPFS 199  
 Db 188 QSGWSQSPHAHGYLDSKFPNQDNLKQMYCRNPDGERPP-----W-----CF 227  
 QY 200 TRVPQMLLVGFASFVMENVRSPVTMCLQDQTSPPPERGQFVC 241  
 Db 228 TTDPN-----KRWERFCDIP-----RCTIPPPSGPTVQC 256

PLBO

Plasmin (EC 3.4.21.7) precursor - bovine

N;Alternate names: plasminogen

C;Species: Bos Primigenius taurus (cattle)

C;Date: 30-Sep-1987 #sequence revision 28-Apr-1995 #text\_change 09-Jul-2004

C;Accession: S45046; A2835; T45961; S03735

R;Berglund, L.; Andersen, M.D.; Petersen, T.E.

Submitted to: the EMBL Data Library, May 1994

A;Title: Cloning and characterization of the bovine plasminogen cDNA.

A;Reference number: S45046

A;Accession: S45046

A;Molecule type: mRNA

A;Residues: 1-812 &lt;BER&gt;

A;Cross-references: UNIPROT:P06868; EMBL:X9402; NID:9494962; PID:CAA55939.1; PID:949496

A;Reference number: S03735; MUID:85203906; PMID:3846532

A;Experimental source: liver

A;Note: it is uncertain whether Met-1 or Met-8 is the initiator

R;Schaller, J.; Moser, P.W.; Dannegger-Muller, G.A.K.; Rosselet, S.J.; Kampfer, U.; Rickli

Eur. J. Biochem. 149, 267-278, 1985

A;Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasmi

A;Reference number: A25835; MUID:85203911; PMID:6148961

A;Status: translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 706-743, 'R', 745-812 &lt;MAL&gt;

A;Cross-references: GB;K0295; NID:9163551; PID:AA30714.1; PID:9163552

R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, B.E.; Lergier, W.; Manneberg, M.;

Eur. J. Biochem. 114, 465-470, 1981

A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, t

A;Reference number: S03735; MUID:81212097; PMID:7238497

A;Accession: S03736

A;Molecule type: protein

A;Residues: 27-83 &lt;BRU&gt;

C;Function:

A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va

ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act

A;Pathway: fibrinolysis

C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;

C;Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma;

P;1-26/Domain: signal sequence #status predicted &lt;STC&gt;

A;Reference number: S03735; MUID:81212097; PMID:7238497

A;Accession: S03736

A;Molecule type: protein

A;Residues: 27-83 &lt;BRU&gt;

C;Function:

A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va

ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act

A;Pathway: fibrinolysis

C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;

C;Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma;

P;8-103/Domain: activation peptide #status experimental &lt;PRO&gt;

F;27-103/Domain: activation peptide #status experimental &lt;PRO&gt;

F;104-583, 584-812/Domain: plasmin chain A #status experimental &lt;PRO&gt;

F;110-188/Domain: kringle homology &lt;KR1&gt;

F;192-269/Domain: kringle homology &lt;KR2&gt;

F;282-359/Domain: kringle homology &lt;KR3&gt;

F;384-461/Domain: kringle homology &lt;KR4&gt;

F;459-564/Domain: kringle homology &lt;KR5&gt;

F;584-812/Domain: plasmin chain B #status experimental &lt;PRO&gt;

F;584-805/Domain: trypsin homology &lt;TRY&gt;

F;60-68, 110-188, 131-171, 159-183, 192-269, 195-323, 213-252, 241-264, 282-359, 303-342, 331

bonds; #status predicted

F;315/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;624, 667, 767/Active site: His, Asp, Ser #status predicted

Query Match 7.8%; Score 105; DB 1; Length 812;

Best Local Similarity 18.3%; Pred. No. 0\_017; Indels 120; Gaps 17;

Matches 55; Conservative 42; Mismatches 83; Indels 120; Gaps 17;

QY 5 LIGFAREVVSADSHRCRCLASACINAADFDFGFECESSVMYVPUDEACTINTEDRLRDLFVD 64

Db 40 LFLSLRKQVAARSVECAAKC-EAET-NFICRAFOYHSKQDQCVMAENSKTSP--IA 67

QY 65 EHEDTVIYLDNNCAGCCHWIFDNFKSGILNDQDFAIAQCYAPVYQVAVEG 119

Db 66 RMRDVLVLFKRYLSECKTGNGKNYRGTTSKKSGVQICQKWSVSSPHIPKYSPEKPLAG 127

QY 120 RQ-----LSDLDHREGELSECELCTQ-----RLSNTANDFNC 155

Db 128 LHENYCRNPDNDKGPWCYTIDPTEFRDYCDPECDECCHMCSGERHEYEGKISKMSIEC 187

QY 156 KS-----FMSNLTRAS-CVLSDESPPLGRANLAEVPGWTVFESRGVPFS 199

Db 188 QSGWSQSPHAHGYLDSKFPNQDNLKQMYCRNPDGERPP-----W-----CF 227

QY 200 TRVPQMLLVGFASFVMENVRSPVTMCLQDQTSPPPERGQFVC 241

Db 228 TTDPN-----KRWERFCDIP-----RCTIPPPSGPTVQC 256

QY 228 TTDPN-----KRWERFCDIP-----RCTIPPPSGPTVQC 256

Q



Qy	132 GELSECEELCTQRLSIVTANDPNCKSPMYSNLTRSCVLSRS	174
Db	408 VENQDCWSLCVN-----SKVRCLELSFSTTSNOCLLTLKS	444
RESULT 14		
PLHU	Plasmin (EC 3.4.21.7) precursor [validated] - human	
N; Contains: angiotatin; microplasmin; plasminogen	N; Contains: Homo sapiens (man)	
C; Species: Homo sapiens (man)	C; Date: 24-Apr-1984 #sequence revision 02-Dec-1994 #text-change 09-Jul-2004	
C; Accession: A55229; 15242; A26646; 162738; 184609; S03735; A00829; A04627; A04625; A04	C; Accession: A55229; 15242; A26646; 162738; 184609; S03735; A00829; A04627; A04625; A04	
R; Petersen, T.B.; Martzen, M.R.; Ichinose, A.; Davie, E.W.	R; Petersen, T.B.; Martzen, M.R.; Ichinose, A.; Davie, E.W.	
R; Biochim. Chem. 265, 6104-6111, 1990	R; Biochim. Chem. 265, 6104-6111, 1990	
A; Title: Characterization of the gene for human plasminogen, a key proenzyme in the fibrinolytic system	A; Title: Characterization of the gene for human plasminogen, a key proenzyme in the fibrinolytic system	
A; Reference number: A35229; MUID:9020879; PMID:218848	A; Reference number: A35229; MUID:9020879; PMID:218848	
A; Accession: A35229	A; Accession: A35229	
A; Molecule type: DNA	A; Molecule type: DNA	
A; Residues: 1-810 <PRT>	A; Residues: 1-810 <PRT>	
A; Cross-references: UNIPROT:P00747; UNIPROT:Q9UBQ9; UNIPROT:Q9UM12; GB:J05286; GB:M34276	A; Cross-references: UNIPROT:P00747; UNIPROT:Q9UBQ9; UNIPROT:Q9UM12; GB:J05286; GB:M34276	
A; Experimental source: leukocyte; lung fibroblast	A; Experimental source: leukocyte; lung fibroblast	
R; Malfatti, N.; Bruno, P.; Pontoglio, M.; Candiani, G.; Maroni, G.; Ottolenghi, S.; Tardieu, P.	R; Malfatti, N.; Bruno, P.; Pontoglio, M.; Candiani, G.; Maroni, G.; Ottolenghi, S.; Tardieu, P.	
A; Title: Definition of the transcription initiation site of human plasminogen gene in leukocytes	A; Title: Definition of the transcription initiation site of human plasminogen gene in leukocytes	
A; Reference number: I5242; MUID:91097523; PMID:2268308	A; Reference number: I5242; MUID:91097523; PMID:2268308	
A; Accession: I5242	A; Accession: I5242	
A; Status: translated from GB/EMBL/DBJ	A; Status: translated from GB/EMBL/DBJ	
A; Molecule type: DNA	A; Molecule type: DNA	
A; Residues: 1-16 <MAIL>	A; Residues: 1-16 <MAIL>	
A; Cross-references: GB:MG62890; NID:9190032; PIDN:AAA36454.1; PID:9553613	A; Cross-references: GB:MG62890; NID:9190032; PIDN:AAA36454.1; PID:9553613	
R; Forbrig, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.	R; Forbrig, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.	
FEBS Lett. 213, 254-260, 1987	FEBS Lett. 213, 254-260, 1987	
A; Title: Molecular cloning and characterization of a full-length cDNA clone for human plasminogen	A; Title: Molecular cloning and characterization of a full-length cDNA clone for human plasminogen	
A; Reference number: A26646; MUID:87162490; PMID:300813	A; Reference number: A26646; MUID:87162490; PMID:300813	
A; Accession: A26646	A; Accession: A26646	
A; Molecule type: mRNA	A; Molecule type: mRNA	
A; Residues: 1-471, 'D', 473-810 <FOR>	A; Residues: 1-471, 'D', 473-810 <FOR>	
A; Cross-references: GB:X05199; NID:935530; PIDN:CAA28831.1; PID:935531	A; Cross-references: GB:X05199; NID:935530; PIDN:CAA28831.1; PID:935531	
A; Experimental source: liver	A; Experimental source: liver	
R; Malfanti, D.P.; Sadler, J.E.; Davie, E.W.	R; Malfanti, D.P.; Sadler, J.E.; Davie, E.W.	
Biochemistry 23, 4243-4250, 1984	Biochemistry 23, 4243-4250, 1984	
A; Title: Characterization of a complementary deoxyribonucleic acid coding for human and bovine plasminogen	A; Title: Characterization of a complementary deoxyribonucleic acid coding for human and bovine plasminogen	
A; Reference number: 145961; MUID:85023311; PMID:6148961	A; Reference number: 145961; MUID:85023311; PMID:6148961	
A; Status: translated from GB/EMBL/DBJ	A; Status: translated from GB/EMBL/DBJ	
A; Molecule type: DNA	A; Molecule type: DNA	
A; Residues: 367-419 <MAIL3>	A; Residues: 367-419 <MAIL3>	
A; Cross-references: GB:K02921; NID:9190110; PIDN:AAA60133.1; PID:9190111	A; Cross-references: GB:K02921; NID:9190110; PIDN:AAA60133.1; PID:9190111	
A; Accession: I84609	A; Accession: I84609	
A; Status: translated from GB/EMBL/DBJ	A; Status: translated from GB/EMBL/DBJ	
A; Molecule type: DNA	A; Molecule type: DNA	
A; Residues: 292-471, 'D', 473-810 <MAIL2>	A; Residues: 292-471, 'D', 473-810 <MAIL2>	
A; Cross-references: GB:K02922; NID:9190112; PIDN:AAA60124.1; PID:9387031	A; Cross-references: GB:K02922; NID:9190112; PIDN:AAA60124.1; PID:9387031	
A; Accession: I84609	A; Accession: I84609	
A; Status: translated from GB/EMBL/DBJ	A; Status: translated from GB/EMBL/DBJ	
A; Molecule type: mRNA	A; Molecule type: mRNA	
A; Residues: 292-471, 'D', 473-810 <MAIL2>	A; Residues: 292-471, 'D', 473-810 <MAIL2>	
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A; Accession: I84609	A; Accession: I84609	
A; Status: translated from GB/EMBL/DBJ	A; Status: translated from GB/EMBL/DBJ	
A; Molecule type: mRNA	A; Molecule type: mRNA	
A; Residues: 292-471, 'D', 473-810 <MAIL2>	A; Residues: 292-471, 'D', 473-810 <MAIL2>	
A; Cross-references: GB:K02922; NID:9190112; PIDN:AAA60124.1; PID:9387031	A; Cross-references: GB:K02922; NID:9190112; PIDN:AAA60124.1; PID:9387031	
A; Accession: I84609	A; Accession: I84609	
A; Status: translated from GB/EMBL/DBJ	A; Status: translated from GB/EMBL/DBJ	
A; Molecule type: mRNA	A; Molecule type: mRNA	
A; Residues: 292-471, 'D', 473-810 <MAIL2>	A; Residues: 292-471, 'D', 473-810 <MAIL2>	
A; Cross-references: GB:K02921; NID:9190110; PIDN:AAA60133.1; PID:9190111	A; Cross-references: GB:K02921; NID:9190110; PIDN:AAA60133.1; PID:9190111	
A; Accession: I84609	A; Accession: I84609	
A; Status: translated from GB/EMBL/DBJ	A; Status: translated from GB/EMBL/DBJ	
A; Molecule type: mRNA	A; Molecule type: mRNA	
A; Residues: 292-471, 'D', 473-810 <MAIL2>	A; Residues: 292-471, 'D', 473-810 <MAIL2>	
A; Cross-references: GB:K02922; NID:9190112; PIDN:AAA60124.1; PID:9387031	A; Cross-references: GB:K02922; NID:9190112; PIDN:AAA60124.1; PID:9387031	
A; Accession: I84609	A; Accession: I84609	
A; Status: translated from GB/EMBL/DBJ	A; Status: translated from GB/EMBL/DBJ	
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A; Title: Primary structure of the B-chain of human plasminogen	A; Title: Primary structure of the B-chain of human plasminogen	
A; Reference number: A04627; MUID:7725245; PMID:142009	A; Reference number: A04627; MUID:7725245; PMID:142009	
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Eur. J. Biochem. 50, 499-504, 1975	Eur. J. Biochem. 50, 499-504, 1975	
A; Title: Structural relationship between "glutamic acid" and "lysine" forms of human plasminogen	A; Title: Structural relationship between "glutamic acid" and "lysine" forms of human plasminogen	
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Eur. J. Biochem. 50, 499-504, 1975	Eur. J. Biochem. 50, 499-504, 1975	
A; Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen that contains the primary structure of the B-chain of human plasminogen	A; Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen that contains the primary structure of the B-chain of human plasminogen	
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Qy 120 RQLSBEELDISFEGLE-----1SECEELCTQ----- 144
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Qy 145 --RIVSTANDFNCKS-----FMWSULTRS-CVLSRSRSPRGRANIAEV 186
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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A;Map position: 2
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Qy 76 NCAGGE 81
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8

5 LVGFAREVVSADSVRCLSACLNAFDTEGFECESMYYPVDAECILNTEDR-----LDRP 59

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GenCore version 5.1.6  
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On protein - protein search, using SW model

Run on: March 31, 2005, 01:56:09 ; Search time 177 Seconds

Post-processing: Minimum Match 0% ; (without alignments)

Database: US-10-771-708-11 ; 723.276 Million cell updates/sec

Perfect score: 1354  
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 Bseqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% ; (without alignments)

Listing first 45 summaries

Database: UniProt 03-\* ; (without alignments)

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	19.4	2	2021	020167
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5	160	11.8	522	017347
6	157	11.6	1494	07PTE3
7	153.5	11.3	398	022902
8	138	10.2	1549	08MK23
9	138	10.2	1549	09BMD5
10	138	10.2	1557	09BMD5
11	138	10.2	1557	09V5X3
12	126	9.3	351	021782
13	125	9.2	774	09V9X1
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15	8.9	7.4	2	09VAG2
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19	119.5	8.8	633	07QBU4
20	118.5	8.8	695	2
21	116	8.6	790	1
22	115	8.5	805	2
23	113	8.3	833	2
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25	105	7.8	812	1
26	104	7.7	810	1
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DT 01-DEC-2001 (TREMBREL, 19, Last sequence update)	
DT 01-OCT-2003 (TREMBREL, 25, Last annotation update)	
DB Hypothetical protein C34G6_6;	
GN Name=C34G6_6; ORName=C34G6_6;	
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OX	
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RC STRAIN=Bristol N2;	
RT "Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology. The <i>C. elegans</i> Sequencing Consortium.";	
RL Science 282:2012-2018(1998).	
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RA Langston Y., Rohlfing T.;	
RT "The sequence of <i>C. elegans</i> cosmid C34G6_6."	
RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.	
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RC STRAIN=Bristol N2;	
RA Waterston R.;	
RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.	
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RG WormBase Consortium;	
RL Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.	
DR EMBL: U07407; AAB52479.2; -.	
DR PIR: C87789; C87789.	
DR WormBase: WBGene0016422; C34G6_6.	
DR WormPep: C34G6_6a; CEB9699.	
DR InterPro: IPR001507; Endoglin/CD105.	
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DR InterPro: IPR003609; PAN_app.	
DR Pfam: PF00024; PAN_6.	
DR Pfam: PF00100; zoma_pellucida; 1.	
DR SMART: SM0473; PAN_AP; 6.	
DR SMART; SM0241; ZIP_1.	
DR PROSITE; PS50948; PAN.	
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DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)							
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RC	Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology. The <i>C. elegans</i> Sequencing Consortium.;								
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RA	Waterson N.; Langston Y.; Rohlfing T.;								
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RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[5]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[6]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[7]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[8]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[9]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[10]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[11]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[12]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[13]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[14]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[15]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[16]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[17]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[18]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[19]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[20]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[21]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[22]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[23]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[24]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[25]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[26]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[27]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[28]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[29]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[30]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[31]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.								
RN	[32]	SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterson N.;								

Query Match Best Local Similarity 22.5%; Pred. No. 9.3e-07; Gaps 15; Matches 76; Conservative 38; Mismatches 100; Indexs 124; Gaps 15; Score 168; DB 2; Length 741; Query 5 LVGFAREVVSAADSVIRCLSLCAGLNAAFDTGFECESVMMYVPADECILNTEDRLRDLFV D 64 Db 137 LGGFKKSVTVVRENRCHLSCAKKEP--PVCNSVPHDTLCLSLVEDKRSP-- 188 Db 62 FVSBHEPTVYLDDNCAG-- 15; C--BC 82 Db 191 FKTMLTDLVDFERNCADVSKPPEETLW-- 220 Db 115 VAVGQLQSDDELDSFEGEGLSECEFLCTQRLSVTANDENCSTPMYSNLTSCVLSRS 174 Db 221 VRTFELYLIDESKVTVESSDAQECNQLC-QNNKIGBENPCKAFAYNSKQECHLTASS 279 Db 175 ---RPLGRANLAEVPGWTFESRGVP-----SFTVQMLVGRASPVNVPVVT 222 Db 280 YVGHKGDKRENLAPLNSGEYFPEKYLCLPTNLQCTIASFELVANRMT--SAYKTIASLQH 337 Db 223 MCLQCTSPPEGTGPNFCKSVMY 248 Db 338 ECLSQCMNDAR-----CSSATFV 357

Result 4

Q9XUE5 PRELIMINARY; PRT; 741 AA.

AC Q9XUE5; DT 01-NOV-1999 (Tremblrel. 12, Created)  
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)

DE Hypothetical protein F52B11.3;  
ORName=F52B11.3;

GN OS Caenorhabditis elegansB;  
OC Butyrya; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderrina; Caenorhabditis;  
OX NCBI\_TaxID=6239;  
RN [1] OX NCBI\_TaxID=6239;

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RC MEDLINE:99056613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode *C.elegans*: A platform for investigating biology";  
RT Science 282:2012-2018 (1998).

RN [2]

RP SEQUENCE FROM N.A.

RA STRAIN=Bristol N2;

RA Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

RL EMBL; 282268; CAB05199.1; -.

DR PIR; T22486; T22485.

DR WormBase; WBGene0000926; F52B11.3.

DR WormPep; F52B11.3; CE18723.

DR InterPro; IPR01507; Endoglin/CD105.

DR InterPro; IPR003014; PAN.

DR InterPro; IPR003609; Pan\_app.

DR Pfam; PRO00024; PAN; 4.

DR Pfam; PRO0100; Zona\_pellucida; 1.

DR SMART; SM00473; PAN\_AP; 4.

DR SMART; SM00241; ZP; 1.

DR PROSITE; PS50948; PAN; 4.

DR KW Hypothetical protein.

SQ SEQUENCE 741 AA; 81738 MW; F6BCC96FED7DBC15 CRC64;

Query Match Best Local Similarity 22.5%; Pred. No. 9.3e-07; Gaps 15; Matches 76; Conservative 38; Mismatches 100; Indexs 124; Gaps 15; Score 168; DB 2; Length 741; Query 5 LVGFAREVVSAADSVIRCLSLCAGLNAAFDTGFECESVMMYVPADECILNTEDRLRDLFV D 64 Db 137 LGGFKKSVTVVRENRCHLSCAKKEP--PVCNSVPHDTLCLSLVEDKRSP-- 188 Db 62 FVSBHEPTVYLDDNCAG-- 15; C--BC 82 Db 191 FKTMLTDLVDFERNCADVSKPPEETLW-- 220 Db 115 VAVGQLQSDDELDSFEGEGLSECEFLCTQRLSVTANDENCSTPMYSNLTSCVLSRS 174 Db 221 VRTFELYLIDESKVTVESSDAQECNQLC-QNNKIGBENPCKAFAYNSKQECHLTASS 279 Db 175 ---RPLGRANLAEVPGWTFESRGVP-----SFTVQMLVGRASPVNVPVVT 222 Db 280 YVGHKGDKRENLAPLNSGEYFPEKYLCLPTNLQCTIASFELVANRMT--SAYKTIASLQH 337 Db 223 MCLQCTSPPEGTGPNFCKSVMY 248 Db 338 ECLSQCMNDAR-----CSSATFV 357

Result 5

Q9XUE5 PRELIMINARY; PRT; 522 AA.

AC Q9XUE5; DT 01-7347; (Tremblrel. 05, Created)  
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Hypothetical protein H42K12.3;  
Name=H42K12.3; ORName=H42K12.3;

GN OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderrina; Caenorhabditis;  
OX NCBI\_TaxID=6239;

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RC MEDLINE:99056613; PubMed=9851916;

RT "Genome sequence of the nematode *C. elegans*: a platform for investigating biology. The *C. elegans* Sequencing Consortium. Science 282:2012-2018 (1998)."  
RT "The *C. elegans* genome sequence: a platform for investigating biology. The *C. elegans* Sequencing Consortium. Science 282:2012-2018 (1998)."  
RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RC Waterston R.; Maggi L.; Harper M.; RA Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Wilson R.; RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RC Wilson R.; RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RC WormBase Consortium; RA Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AFO26207; AAB71266.1; -.

DR PIR; T32444; T32444.

DR WormBase; WBGene0019272; H42K12.3.

DR WormPep; H42K12.3; CE1614.

DR InterPro; IPR003014; PAN.

DR InterPro; IPR003609; Pan\_app.

DR InterPro; IPR00084; TSPI.

DR Pfam; PRO0024; PAN; 2.

DR SMART; SM00473; PAN\_AP; 2.

DR SMART; SM00203; TSPI; 1.

DR PROSITE; PS50948; PAN; 2.

DR PROSITE; PS50902; TSPI; 1.

DR Hypothetical protein.

SQ SEQUENCE 522 AA; 58738 MW; C4B804F9A0059180 CRC64;



DT 01-MAR-2004 (TREMBrel, 26, last annotation update)  
 DE CG13207-PC (Cg13207-pd).  
 RN NAME="CG13207"; ORFNames=CG13207;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eutaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydriodea; Drosophilidae; Drosophila.  
 RN NCBI\_TaxID=7227;

[1] SEQUENCE FROM N.A.  
 RX MEDLINE=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides B.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richardson S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,  
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Balilew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernick B.P., Bhandari M., Bolshakov S.,  
 RA Borkova D., Botchkina M.R., Bouck J., Brodtman P., Brottier P.,  
 RA Burttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahake R., Daponte L.B., Davies P.,  
 RA de Pablo J., Delcher A., Deng Z., Mays Z., Mays D., Dew I., Dietz S.M.,  
 RA Dodaon K., Douc L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin R., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W.,  
 RA Fosler P., Lei Y., Levinsky R.A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matteil B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Hervaud J.,  
 RA Hosten D., Houston K.A., Howland T.J., Wei M.H., Ibeagwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levinsky R.A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matteil B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacble J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert H., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klamm I., Simpson M., Skupski M.P., Smith T.,  
 RA Siper E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svartas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu Q., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*,"  
 RL Science 287:2185-2195 (2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426065; PubMed=12537568;  
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Chang E., Dugan S.P., Frise E., Hodges A.,  
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,  
 RA Pacielek J.M., Park S., Preffer B.D., Richards S., Sodergren E.J.,  
 RA Svartas R., Tabor E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,  
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*  
 RT melanogaster euchromatic genome sequence,"  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Kaminker J.S.S., Bergman C.M., Kronmiller B., Carlson J., Svartas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.,  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin: a genomics perspective,"  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bernier B.P.,  
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
 RA Harris N.L., Richter J., Heit G., Nelson C.R., Gabor G.L.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.,  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review,"  
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX EMBL, AR00326, AM68728.2, -.  
 RG FlyBase, Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RL [6]  
 RP SEQUENCE FROM N.A.  
 RX FlyBase, Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RG FlyBase, Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AR00326, AM68728.2, -.  
 DR FlyBase, FBgn001647, nompa.  
 DR GO: GO:0016358; P: dendrite morphogenesis; TAS.  
 DR GO: GO:0009592; P: detection of sound; IMP.  
 DR GO: GO:0007605; P: perception of sound; IMP.  
 DR InterPro; IPR001505; Endoglin/COPD05.  
 DR InterPro; IPR003014; PAN.  
 DR InterPro; IPR003609; Pan\_app.  
 DR Pfam; PF00024; PAN; 4.  
 DR Pfam; PF00100; Zona\_pellucida; 1.  
 DR SMART; SM00473; PAN\_AP; 4.  
 DR SMART; SM00474; ZP1.  
 DR PROSITE; PS50948; PAN; 5.  
 SQ SEQUENCE 1549 AA; 174236 MW; 5C65F4D8A2E7CD2C CRC64;  
 QY Query Match 10.2%; Score 138; DB 2; Length 1549;  
 Best Local Similarity 21.2%; Pred. No. 0.0014;  
 Matches 58; Conservative 43; Mismatches 100; Indels 72; Gaps 13;  
 QY 3 KILVGFAREPVNSADSVHRCGLSACIACNAFDTFGFEGESVMMYPVDAECLMTEDRDRPDRF 62  
 DB 164 KULPSDIKITAANR-SOEDKCN--EFSFVRSANDPDSRSTSCTLRFTRRTHPSLM 219  
 QY 63 VDEHEDTVYLDNNCAGCCHWHDNFKTSGLINDQFQFIAQCGAYPYTQYVAVEGRQL 122  
 DB 220 EDDPNSD-YLLENITCLNAE-----RRCDG--LAVFVKEENKRL 253  
 QY 123 SD--ELDHKPEGLSBCELCTLORLSTVANDFNCFSWFSNLSNTRCSVNSDERS-RPLGR 179  
 DB 254 GGRPEVDF-IPNNWLEECCTMC---IAKAKYCRSVERDPSQKQTSSEEDSISQKD 307  
 QY 180 ANLAEVPGWYTFE-----SRGVFSFTRVQMLLVG-FASSP 213  
 DB 303 ISISSSPTHFVYDVLQDNRANDYPDNSVTSVHLSGRPDTAFQYNSRLGGEFISSE 367  
 QY 214 VMENVPVSYWCLDQTSPPBTGTQFVCKSVMY 246  
 DB 368 ITGR--SLSBCLECLRQ----TSFQCRSAVY 393  
 RESULT 9  
 Q9BMD4 PRELIMINARY; PRT; 1549 AA.  
 AC Q9BMD4  
 AC Q9BMD4; 01-JUN-2001 (TREMBrel. 17, Created)  
 DT 01-TUN-2001 (TREMBrel. 17, Last sequence update)  
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)  
 DE No-mechanoreceptor potential A short isoform precursor.  
 GN Name="nompa";  
 OS Drosophila melanogaster (Fruit fly).  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydriodea; Drosophilidae; Drosophila.  
 RN [1]  
 NCBI\_TaxID=7227;









RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Mungall J.S., Mattioli B., Campbell K.S.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Bettencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.,  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 RT systematic review.";  
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RG FlyBase; PDB; Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RL [6]  
 RP SEQUENCE FROM N.A.  
 RG FlyBase;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 RL [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Dresnick D., Farfan D., Fries E.,  
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Mialda A., Mungall C.J., Nuno J., Paclob J., Paragas V., Park S.,  
 RA Batel S., Bhouamikavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celinker S.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003771; AAF66948; 1; .  
 DR EMBL; AY034725; AAM11078; 1; .  
 DR FlyBase; FBgn0039704; CG7802.  
 DR InterPro; IPR001507; Endoglucanase.  
 DR InterPro; IPR003014; PAN.  
 DR InterPro; IPR003609; Pan\_app.  
 DR Pfam; PF00024; PAN; 3.  
 DR SMART; SM00473; PAN\_AP; 3.  
 DR SMART; SM00241; ZP; 1.  
 DR FROST; PS50948; PAN; 3.  
 DR SEQUENCE; 744 AA; 83086 MW; FD2403A63FF75FFBE CRC64;  
 > Query Match Similarity 8.9%; Score 121; DB 2; Length 744;  
 > Best Local Similarity 23.4%; Pred. No. 0.022; No. 0.022;  
 > Matches 64; Conservative 29; MisMatches 102; Indels 78; Gaps 14;  
 Qy 5 LVGPAERVVSA-----DS-----VHRCLASCLNAFTDFGFECECSVWYVDAEC 48  
 Db 117 LVGF--EIVTGYVFSAPEKLMDSQPGTMLTDCLDTORK---NKTQSVNY--ETGLC 167  
 Qy 49 IINTEIDLDRD-LFVDEBHDIVTIVYIILDNNCAG--CECHWHDNDNKTSGILNDQOFAIA 104  
 Db 168 VLFSAHADQLGGALTQKSPVFTIVAQKSCLAVKCQSRANWYDR----- 211  
 105 QCYAPVYTQYVAVEGRQLSDFDIDHSPFEGLESECBLCTORSVANDFNCKSFMNSLT 164  
 Db 212 -----VQNYKLUKEKRTVSVASRRECEBLC---LGENDFTCRSANYDRTS 254  
 Qy 165 RSCVNSDERSRPLGRANLAEV-PGWTYFESRGVP-----SFRTRVQMLVGFASFVME 217  
 Db 255 GACELSELDRLRTLAGSQAFQVNDGSDYPLEHNICVDESPNKLCKRLPGRILKTVPS-VYQE 313  
 Qy 218 VPSVTVMLQDQTSPPPETGQFNVCKSVMMYME 250  
 Db 314 VSSIDBCRELQINS-----YRCHS--YDYN 338

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